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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

 n.a. database search, using Smith-Waterman algorithm л В. MPsrch\_nn MasPar time 215.75 Seconds 980.525 Million cell updates/sec Tue Dec 9 08:36:34 1997; Run on:

Tabular output not generated.

Title:

1 GAATICGGCCTTCATGGCCT.......AAAAAAAAAAAAAAGGGCCGC 2027 CTTAAGCCGGAAGTACCGGA......TTTTTTTTTTTTTCGCCGGCG >US-08-848-439-1 (1-2027) from US08848439.seq 2027 Description: Perfect Score: N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 ٠. STD Nmatch

142080 seqs, 52183452 bases x

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq28
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28

Variance 6.937; scale 1.430 Mean 9.918; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	No.	97	32	30	60	80	07	07	07	07	90	90	90	90	90	90
	Pred.	1.17e-97	3.43e-32	5.69e-30	8.73e-09	2.71e-08	2.56e-07	7.77e-07	7.77e-07	7.77e-07	2.34e-06	7.00e-06	7.00e-06	2.34e-06	7.00e-06	7 000-06
	Description	Human gene signature	Human Natriuretic Pep	Human Natriuretic Pep	Oligonucleotide probe	Base substituted E.co	Oligonucleotide probe	Generic DNA sequence	Generic DNA sequence	Base substituted E.co	Generic DNA sequence	Conorio ANA conoc				
	DI	T23535	010572	010572	051746	N81164	051746	070468	070466	N81164	070469	970465	070467	070469	070466	97070
	90	20	~	~	σ	Н	თ	12	13	Н	12	12	12	12	12	;
	Match Length	204	1047	1047	91	204	91	114	114	204	114	114	114	114	114	114
s Ouerv	Match	9.6	4.3	4.1	2.5	2.1	2.0	2.0	2.0	2.0	1.9	1.9	1.9	1.9	1.9	0
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Result	No.	Н	7	М	4	S	ø	7	œ	σ	10	11	12	13	14	ŗ
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Generic DNA sequence 6.09e- Generic DNA sequence 6.09e- Generic DNA sequence 6.09e-	ų 'n	'nί	5.10	4.09	3.13	100	2.27	2.27	2.27	2.27	8.48	1.04	5.96	5.96	5.96	bovine VEGF-1 5.96	ascular endot 5. ascular endot 5.	EGF-164 codin 5.96e	IS	SULT 1 T23535 standard; cDNA to mRNA; 204 BP.			; relative abundance; frequency;	diagnosis; de							near 11 ANGO near	man con reparin	in specific human		ementary strand or the corresp	s one of the 7837 "GS" sequences	able to hybridise to part of	Claimed. The GS (Gene Signature)	is of cDNA was initiated from the	the sole primer. Since the 3'-	with specific mRNAs. Each librar	e relative abundance	issue irom which it was derived.	so in a conditionally can be probes derived from the GS	abnormal cell function or for	; 35 G; 55 T;
07 07 10 10 10	27,7	65	12	22	7 7	8 2	23.	10	133	21	11	- 4 LC	22	0.5	7 Z	22	96	79	ALIGNMENT	204			RNA	tion							7, -7	func	corr	2		rise	h 1s	1.50	thes	88	dise	acc	ar t	and	sing S.	29 C
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                                                                                              tecectgeettttgeaegtttgeatececageattteetgagttataaggeeacaggag 120
                                                                                                                         9
                          Gaps
                                                                                                                                                                                                                                              09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase; hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Natilizatic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.
The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having quantl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce
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     Length 204;
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                                                                                                                                                                                                                                                                                                                                                                       A,B and
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "GC and protien kinase activity"
Modified -site 24..26
/label= N-glycos_site
Modified -site 35..37
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     'note- "binds natriuretic peptides
                                                                                                                                                                            antaaaatcatgaatattttta 202
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Q10572 standard; DNA; 1047 BP.
Q10572;
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      99.08
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Chang M, Goeddel D, Lowe D;
WPI; 91-036711/05.
N-PSDB; Q10324.
                                                                                                                                                                                                                                                                                                                                                                                                            /label= cytoplasmic domain
              Best Local Similarity 99.5%;
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label = N-glycos_site
Modified -site 195..197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= N-glycos_site
Modified -site 277..279
/label= N-glycos_site
Modified -site 349..351
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Modified -site 600..602
/label N-glycos_site
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                                                                                                                                                                                                                                                                                                                                                                                 456..456
                                                                                                                                                                                                                                                                                                           Peptide 1..22
/label= signal sequence
Protein 12
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22-JUN-1990; U03586.
23-JUN-1989; US-370673.
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Modified -site 161..1
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Modified -site 244..2
                                                                                                                                                                                                                                                                                                                                         /label- mature NPBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriluretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can also be prepd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    785 ATAAAAATGATGATGACAACGAC-ATAATGGAAACGCTTTGTAAAAATGATTTT-GCACT
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4.3%; Score 88; DB 2; Length 1047
Best Local Similarity 8.4%; Pred. No. 3.43e-32;
Matches 83; Conservative 278; Mismatches 618; Indels
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The sequence was derived from the DNA encoding natriuratic peptide receptor B, NPRB, having quanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuratic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                        Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment of
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Larity 9.1%; Pred. No. 5.69e-30;
Conservative 286; Mismatches 627; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
| 1abel = extracellular domain
| note = "binds natituretic peptides A,B and C]"
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/note- "GC and protien kinase activity"
wodified -site 24..26
                                          1015 nnnnnrgdvnmkgkgkmrtywnngnrk 1041
                                                                                  1622 CATCAGCTCCAGACTGAGACTCAGTGT 1648
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                                                                                                                                                                       Q10572 standard; DNA; 1047 BP
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22-JUN-1990; U03586.
23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
Chang M, Goeddel D, Lowe D;
WPI; 91-036711/05.
N-PSDB; Q10324.
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Modified -site 600..602
/label N-glycos_site
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Modified -site 277..279
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Modified -site 161..163
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Modified -site 349..351
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/label- signal sequence
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Modified -site 35..37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ndrntdnvnwamgdndsgdnnnaahysganknnwwtgrnnnwvkgannsdnnncandndd 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ryhkgagsrntnsnrgssygsnmtahgkynnnantghnkgnvvankhvnkkrnnntrnvn 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nnnkhmrdvnnnhntrnngacndnnnncnvtnycnrgsnndnnnndsnnndwmnrysnnn 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ntannnns-gnnnnttgmnaadvysngnnnnnnnnssgnnynngndnsnknnvnkvrngn 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sdnvgntansanstnmnvvtnnndnytcndanndnndvykvntngdaymvvsgnngrngn 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510 CTICATGACCAGCGGATCCAAGCGCCGGCCTGCTCCAGCACCTCCTTCATGGTCTCGTG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mnnyannnnknvnnrtnaynnnkrkanannynnnnhsvannnkrgntvnanandsvtnyn 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450 GCCCAGCAGGTTGGGCAGCCGCATGTTCTGGTATTCGATGCCGTGGCACAGCTGCAGGTT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCCGGGATGGGCTTGCAATTGCTGCGCTTGTAGGAGAGTC-GGGCTGGCCAAAGAGGA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rhannnarmananndavssnrnrhrnhdnnrnrngvhtgnvcagvvgnkmnrycnngdtv 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     985 ntasrmnsngnanknhvssttkdandnngcnnnnnrgdvnmkgkgkmrtywnngnrkg 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 CAGGGCCCTGCAGCATCGTGGGCGCGCGCGAGGGGGGCAGAGGGAGCGGAGCCGG 214
                                                                                         :::| :: :: :: | :: | : | : | : | : | :: | :: | :: | :: | :: | | :: | :: | :: | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | 
knyhdndnnngngcvynaasvarnashwrnnnntagavasgn-sakndhyrtnvrtgnsa
                                                                                                                                                                                                                                                                            nkngnnvvtnhghnnwtaraannyndartddrnhyntnngvnnanngsnnsvnhnvyarn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nggnnnathnnrangrnvyncgnnnmnhnnnnnanrnnntngdyvnnyndvngnsnragn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          865 TTATCTCCTTCACTTTTATTTTCAGTGCAAAATCATT-TTTACAAAGCGTTTCCATTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAACGGTCGCACTCAAGCATGTCGGGCCAGGGGAAGCCGAAGGCGGACATGACCGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dnvkgmannhnsnnsshgsnkssncvvdsrnvnkntdygnasnrstannddnnanyakkn
                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTCTCTCTCTCCCCCTTCTGCCACCGCTTCACCGAGGTGATCAC-CAGCTCCCCACCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .043 ITCTGTCCCATGACCAGATAGGCCGCGTTGATGTCGTTCATCTCCTCACAGGTGCACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  983 AAGCTGTCTTTGAGCCACAGCACCGATTTCTTCAGGTCCCTTTCGGACACACCGTTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              923 TIGIAAAIGGICTIGCICTIGGICTCCAGGAIGAIII-IGGIAICI-CGGIIGAIGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rnynrnsndrtnnnnnnnnnnrcwandnanrndngnnkgnnrrnnknggtsnndnnnr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease dlagnosis;
ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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Q51746;
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Introducing random point mutations into nucleic acods -

Introducing random point mutations into nucleic acods -

by prepn of single stranded template, annealing a primer, elongation,

misincorporation, completion of molecules and screening.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of

E coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligoniclectide was hybridised to

c it to generate a popn of DNA molecules which terminate at all

possible nucleotide positions within a specified region. The

variable 3' ends generated in this way are used as primers for

reverse transcriptase. Nucleotides are missincorporated by the

c transcriptase and the molecules are completed to forms that can be

amplified and then expressed in a suitable host-vector system.

C The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    5 ccggcgssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhhvhyhvyvsvc 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-Nov-1990 (first entry)
asse substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli
                                                                                                                                          New oligo:nucleotide probes specific for Mycobacteria – used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 Others;
                                                                                                                                                                                                            Oligonucleotide probe MK14'A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P. Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 204;
                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                      2.2%; Score 44; DB 9; Length 91; 8.8%; Pred. No. 8.73e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 T;
                                                                                                                                                                                                                                                                                                       4 T;
                                                                                                                                                                                                                                                                                                                                                         Pred. No. 8.73e-09;
48; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 1; L. Pred. No. 2.71e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 C; 17 G;
                                                                                                                                                                                                                                                                                                       15 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     occurred singularly in any given mutant. See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                     17 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function-multiple cloning site
primer_bind 187..204
                                                                                                                                                                                               Claim 3; Page 14; 23pp; English
                               01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 5
N81164 standard; DNA; 204 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.1%;
Best Local Similarity 11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 A;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19..69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 BP;
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                       91 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                  EP-571911-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP-285123-A.
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                               samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                 199
                                                                                                                                                                                                                                                                                                                                                                             Matches
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Gaps

ö

58; Mismatches 42; Indels

Conservative

78

Matches

dchvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyv 137

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Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 35; 255pp; English.

Q70468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides.This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)62(NNB)7(TGC)(NNB)10Y. X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
138 ybbbvynvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccvch 190
                                          387 GGCCAACCTGCAGCTGTGCCACGGCATCGAATACCAGAAACATGCGGCTGCCCA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1093 GCCCCTTCTGCCACCGCTTCACCGAGGTGATCACCAGCTCCCCACCC 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.56e-07;
44; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 svhsyyvvhvvshhhsvhhvvhhvhhvhvhhvhhvhhvhyhvyv 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probes specific for Mycobacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- 'this sequence represents '2'; 2 can be sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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01-FEB-1994; U00977.

01-FEB-1993; US-13416.

30-DEC-1993; US-176500.

31-JAN-1994; US-189331.

(UNC) UINV NORTH CAROLINA.

FOWIKES DM, KAY BK;

WPI: 94-279739/34.
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                                                                                                                                 LT 6
Q51746 standard; cDNA; 91 BP.
Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                        EP-571911-A.
01-DEC-1993.
24-MAY-1993. 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New oligo:nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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ont yare flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Cother specific peptides generated by these generic sequences are shown in R6151-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonual cotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARS or compans. Comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, andioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resulting proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins of screening a binding domain and an effector domain proteins.

Tromprizing a binding domain and an effector domain bisclosure; Page 35; 255pp; English.

Oldsclosure; Page 35; 255pp; English.

Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)10(TGC)2(NNB)42(NNB)8(TGC)(NNB).

Compressented as follows: X(NNB)10(TGC)2(NNB)42(NNB)8(TGC)(NNB).

That are not specified further. Other generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 CCGCCTCGCCCTTCCCCGGCTCGCGTCGCGGGTCGCGCGCCCACGATG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 bnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 12; Length 114; Pred. No. 7.77e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "this sequence represents '2'; Z can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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FOWIKES DM, RAY BK;
PWDI; 94-279739/34.
P-PSDB; R65152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.0%; S.1%; Iarity 5.4%; Conservative
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Q70466 standard; DNA; 114 BP.
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US-176500.
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Matches 6; Conser
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30-DEC-1993;
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linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARS or compsis. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARS are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 gggywccgagcycgaayycdchvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyr 118
                                                                                                                                                                                                                                                                                                                                                                                    Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                            5 gcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgctgcnnbnnbnnbnnbnnbnnbn 64
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Random point mutations were introduced into the alpha fragment of E.coll beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 T; 108 Others;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lentovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                        65 nbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 TCCTCTTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCC 381
                                                                                                                                                                                                                                                                                  Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 7.77e-07;
57; Mismatches 51; Indels
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                                                                                                                                                                                                                                                                                                                      69; Indels
                                                                                                                                                                                                                                                                                2.0%; Score 40; DB 12; larity 9.1%; Pred. No. 7.77e-07; Conservative 31; Mismatches 69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Best Local Similarity 15.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
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                                                                                                                                                                                                                                                                                                    Local Similarity
les 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
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                                                                                                                                                                                                                                                                                    Query Match
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Matches
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Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.

LT 11 Q70465 standard; DNA; 114 BP. Q70465;

(first entry)

05-APR-1995

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'Z'; Z can

sequence represents  $^{\prime}2^{\prime};$  Z 6, 9 or 12 nucleotides (see

Kay BK;

Fowlkes DM

Location/Qualifiers

Synthetic.

55..60

/\*tag= a /note= "this misc\_feature

sequence of WO9418318-A

comments)

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18-AUG-1994.
01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prowinces DM, ARMY BK);

PT FOWLKES DM, ARMY BK);

PT Identifying proteins or peptide(s) which bind a ligand - by

Identifying proteins or peptide(s) which bind a ligand - by

Screening a recombinant vector library expressing fusion proteins

PT Comparising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English,

CC (7046) is a generic DNA sequence used to generate random TSAR peptide

CC (TGC) (NNB) 6Z (NNB) 2(TGC) (NNB) 14 (TGC); Y. X and Y are flanking restriction

Sites (X is not the same as Y) that are not specified further. This

CC (TGC) (NNB) 6Z (NNB) 14 (TGC) (NNB) 14 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
119 rsvkydccynachhddhyvybbbvynvhnhnncncccbnnhvchnvhbnnhrnwayvrhd 178
                                  595 TGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCGCCTTCGGC 654
                                                                                                                                                                                                                           Generic DNA sequence to generate a random TSAR peptide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 114;
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Pred. No. 2.34e-06;
32; Mismatches 71; Indels
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/note= "this sequence represents '2'; Z can be
sequence of 6,9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 G;
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 55..60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UXNC-) UNIV NORTH CAROLINA.
FOWLKS DM, KAV RK
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Q70469 standard; DNA; 114 BP
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Best Local Similarity 7.2%;
                                                                                                                                                                                                           (first entry)
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                                                                    179 arrddvhc 186
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PI FOWINGS DM, KAY BK;

WPI: 94-27939/34.

P-PSDB: R65150 and R65151.

PT Identifying proteins or peptide(s) which bind a ligand - by
recening a recombinant vector library expressing fusion proteins

PT Comprising a binding domain and an effector domain

PS comprising a binding domain and an effector domain

Disclosure; Page 35: 255pp: English.

COMO465 is a generic DNA sequence used to generate random TSAR (Totally

COMO465 is a generic DNA sequence used to generate random TSAR (Totally

CSYNTHETIC Affinity Reagants) peptides. This generic formula can also be
crepresented as follows: X(NNB)6(TGC)(NNB)11Z(NNB)14(TGC)(NNB)3Y. X

CC and Y are flanking restriction sites (X is not the same as Y) that are
corporated for their generated by these generic sequences are shown in

CC Specific peptides generated by these generic sequences are shown in

CC Comprising at least two functional regions. - a binding domain with

CC Affinity for a ligand and a second effector peptide portion that is

CC Chemically or biologically active. They may further comprise a linker

CC Chemically or biologically active moiety es metal ion,

CC That the expressed peptide contains 2 or 4 cysteine residues positioned

CC That the expressed peptide contains 2 or 4 cysteine residues

CC Comprise a chemically or biologically active moiety, es. metal ion,

CC deliver a chemically or biologically active moiety, es. metal ion,

CC deliver a chemically or biologically active moiety, es. metal ion,

CC addiostope, peptide, toxin or enzyme, to the specific target or on the

CC coll. They can also replace the function of macromolecules, eg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 banbanbanbanbanbtgcanbanbanbanbanbanbanbanbanbanbanbanban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing infect and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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070467;
070467;
05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 CCTCTTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 7.00e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.9%;
Similarity 4.5%;
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins promptising a binding domain and an effector domain proteins page 35; 255pp; English.

Disclosure: Page 35; 255pp; English.

Disclosure: Page 35; 255pp; English.

CC Synthetic Affinity Reagents) peptides. This generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generate formula can also be represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)12.

CC Synthetic Affinity Reagents) peptides (X is not the same as Y) that are not specified further. Other generic sequences are shown in 700466-68.

CC Ther specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in a R65151-54. TSARs are concatenated by these generic sequences are shown in Affiliaty for a ligand and a second effector peptide portion that is chemically or a ligand and a second effector peptide portion that is chantche expressed peptide contains 2 or 4 cysteine residues so that the expressed peptide contains 2 or 4 cysteine residues so that the expressed peptide contains 2 or 4 cysteine residues so that the expressed peptide or variant residues. These residues comprise, engines are also designed a companie, comprise a peptide, toxin or enzyme, to the specific target or on the concatenated and also replace the function of macromolecules, eg.

CC comprise and slow replace the function of macromolecules, eg.

CC concatenated and an also replace the function of macromolecules, eg.

CC concatenated and an also replace the function of macromolecules, eg.

CC concatenated and an also replace the function of macromolecules, eg.

CC concatenated and an also replace the function of macromolecules, eg.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 GCGGCCTCGCCCTTCCCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCCACGAT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss. Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 GCTGCAGGGCCCTGGCTGCTGTTTCCTCGCACTGCTGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               defection in a screening process. P; 0 A; 2 C; 2 G; 2 T;
                                                                                              /*tag= a /note= "this sequence represents '2'; Z can be sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 7.00e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38;
                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
55..60
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Q70469 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                 (UYNC-) UNIV NORTH CAROLINA.
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                                                                                                                                                                                                    US-013416
                                                                               55..60
                                                                                                                                                                                                                   US-176500
                                                                                                                                                                                                                                    US-189331
                                                                                                                                                                                                                                                                 Kay BK;
                                                                                                                                                                                       T000D
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Best Local Similarity
                                                                                                                                                                                                                                                                  Fowlkes DM, Kay B
WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               direct and rapid do Sequence 114 BP;
                                                                                                                             seguence of 6, 9
                                                                                                                                                                                                                                                                                               P-PSDB; R65153
                                                                                 misc_feature
                                                                                                                                                                                     01-FEB-1994;
                                                                                                                                                                                                     01-FEB-1993;
                                                                                                                                                                                                                     30-DEC-1993;
                                                                                                                                                                                                                                    31-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                         WO9418318-A.
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This generic formula can be represented as follows: X(TGC)(NNB)52 (NNB)20 (TGC)(NNB)52 (NNB)20 (TGC)(NNB)52 (NNB)20 (TGC)(NNB)52 (NNB)20 (TGC)(NNB)52 (NNB)20 (TGC)(NNB)52 (NNB)20 (TGC)(NNB)52 (NNB)20 (TGC)(NNB)20 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and meffector domain Disclosure; Page 35; 255pp; Engilsh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         540 CAGGAACTICITGGTGTCCGGGTGGCACTGCTTCATGACCAGCGGGATCCAAGCGCCGGC 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR, totally synthetic affinity reagent; synthetic; binding domain,
effector domain, concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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Pred. No. 2.34e-06;
32; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 T;
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/note= "this sequence represents 'Z'; Z can be sequence of 6,9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "this sequence represents', 2 can be
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G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      070466 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                 01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UXNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.9%;
Similarity 7.3%;
8; Conservative
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01-FEB-1993; US-013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 94-279739,
                                                                                                                                                                  18-AUG-1994.
01-FEB-1994;
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                                                                                            comments)"
WO9418318-A.
                                                sednence of
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US-013416

fusion proteins

expressing

a recombinant vector library

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Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins PT Identifying proteins are comprising a bluding domain and an effector domain bisclosure; Page 35; 255pp; English.

Disclosure; Page 35; 255pp; English.

CO 70466 is a generic DNA Sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows:X(NNB)[CGC)(NNB)10(TGC)2(NNB)4Z(NNB)8(TGC)(NNB) CCC Synthetic Affinity Reagents) peptides generic sequences are shown in R65151-54. TSARS are concatenated by these generic sequences are shown in R65151-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues. These positioned in, or flanking, the unpredicted or variant residues. These costiones confer some degree of conformational rigidity to the peptides.

CCC for the TSARS or compens. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal contains and therefore circumvent the need for complex methods of hybridoma formation or enzyme, to the specific target or monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production.

CCC The TSARS are easily characterised and have designed activity allowing distorts and read or the constant of the call of the constant of the complex methods of hybridoma formation or in vivo antibody production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513 CTGCTTCATGACCAGCGGGATCCAAGCGCCGGCCTGCTCCAGCACCTCCTTCATGGTCTC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 btgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgctgcnnbnnbnnbnnbnnnnnn 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 banbanbanbanbanbanbanbtgcanbanbanbanbanbanbanbanb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 GTGGCCCAGCAGGTTGGGCAGCCGCATGTTCTGGTATTCGATGCCGTGGCAC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying proteins or peptide(s) which bind a ligand - by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection in a screening process.
P; 0 A; 4 C; 4 G; 4 T;
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Q70468 standard; DNA; 114 BP.
                          31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
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Fowlkes DM, Kay BK;
WPI; 94-279739/34.
P-PSDB; R65154.
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Matches 10; Conservative
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01-FEB-1993; US-0134
                                                                                                          Fowlkes DM, Kay B WPI; 94-279739/34.
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31-JAN-1994;
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Distribute and the sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)17(TGC)(NNB)10V. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so
                                                                                                                                                                                                                                                                                                                                                                          that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
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                      comprising a binding domain and an effector domain
Disclosure: Page 35: 255pp; English.
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ilarity 4.5%;
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                                                                                                                                                                                                            Smith-Waterman algorithm
                                                                                                                              Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U. Distribution rights by IntelliGenetics, Inc.
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   179:EST179
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High quality sequence stop: 390.
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
7e1: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1550 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 424.
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             Homo sapiens
Eukaryotes; Metazoa; Chordata;
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases i to 462)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M.
Parsons, J., Rifkin, L., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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WSNWSNGAYCAYYINYINCCNGCNACNGARGARGCNCCNAARGINTGYGARGCNTGYAAR
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/lab_host="DH10B (ampicillin resistant)"
/lab_host="10B (ampicillin resistant)"
/lab_host="10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="346028"
/clone_llb="Soares fetal heart NbHH19W"
/sex="unknown"
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108; Mismatches 8:
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1 Similarity 58.0%; Pred. No. 0.
266; Conservative 108; Mismatc
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mm97f07.rl Stratagene mouse heart (#937316) Mus musculus cDNA clone 536389 5' similar to TR:G1151260 G1151260 TRANSMEMBRANE RECEPTOR.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schallenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 315 286 1810
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:323325
                                                                                                                                  04-OCT-1996
364 caagagcaagaccatttacaagctgaacggtgtgtccgaaagggaccttgaagaaatcgg
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/sex="pooled"
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/lab_host="SOLR (kanamycin resistant)"
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High quality sequence stops: 355
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                      178
                                                                                                                               238
          teetgtgetegetettegeeetgtetgtetegaegaeetagatgagaeeateeageegt 119
                                        TYYTHIGYWSNYTHTTYGCNCCNGTHTGYYTHGAYGAYYTHGAYGARACNATHCARCCNT 340
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Eukaryotte; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 406)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Hollman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Y12805.r1 Homo sapiens cDNA clone 159560 5'
H16121
9880941
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WashU-Merck EST Project
Washington University School of Medicine
                                                                                                                  Score 304; DB 72;
Pred. No. 0.00e+00;
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/organism="Homo sapiens"/clone="220525"
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Fax: 314 286
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 321
Source: IMAGE Consortium, Lini.
This clone is available royalty-free through Lini; contact the IMAGE Consortium (info@image.lini.gov) for further information.
Location/Qualifiers
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2e76gl0.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone
364962 5'.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 414)
1 (lases 1 to 414)
1 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                         cccaggacaacgacctttgcatccccttcgctagcagcanccacctcctgccagccaccg
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WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                               'n
                                                                                                                                                                                                   Length 406;
                                                                                                                                                                others
                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                   Score 279; DB 61;
Pred. No. 0.00e+00;
89; Mismatches 60;
                                                                                                                                                              ų
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                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                               /clone="159560"
94 c 10
                                                                                                                                                                                                   Query Match 38.0%;
Best Local Similarity 58.9%;
Matches 221; Conservative
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H14917 27-JUN-1995
yl26d03.rl Homo sapiens cDNA clone 159365 5' similar to SP:A45054
A45054 Fz-1-PUTATIVE INTERCELLULAR SIGNAL TRANSDUCER OR TRANSMITTER
                                                                                                                                                                                                                                                                                                                                                                                                                             .,
Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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human clone-159365 library-Soares breast 3NbHBst vector-pT7T3D
(Pharmacia) with a modified polylinker host-bH10B (ampicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 gacattaatggaaacgctttgtaaaaatgattttgcacttgaaaattnaaagtgaaagga
                                                                                                                                                                                                                                                                                                                                                                                                  Score 277; DB 156; Length 414;
Pred. No. 0.00e+00;
85; Mismatches 54; Indels 5;
                                                                                                                                                                                                                                                                                                                              (ampicillin resistant)"
                                                                                                                                                                                                                                                                                        /clone_lib="Soares fetal heart NbHH19W"
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                                                                                                                                                                                                                                                                                                                                                           82
                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                   weeks"
                                                                Location/Qualifiers
1..414
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                                                                                                                                                                                                                                                                                                                  /dev_stage="19 we
/lab_host="DH10B
                                                                                                                                                                                                                                                                                                                                                           95
                                                                                                                                                                                                                                                                          /clone="364962"
                                                                                                                                                                                                                                                                                                        /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                               37.7%;
|larity 60.9%; |
|Conservative |
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house mouse.
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomda; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopterygli; Choanata; Terrapoda; Amniota; Mammalla; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 344)
11 liar, Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stops: 59
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ginaaaggaccgctgcgccccggtcatgtccgncttcggtttcccctgggcccgganatg 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 aagcccatcccggtcaacctgcagctgtgccacggcatcgaataccagaacatgcggctg 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cccgtctgcctngatgacctagacgagaccatccagccatgccacttgntctggtntcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 242; DB 61; Length 344,
Pred. No. 5.47e-272;
69; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/clone="159365"
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                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                 The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.0%;
Best Local Similarity 60.1%;
Matches 205; Conservative
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                                                                                                                    Homo sapiens
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mRNA EST 05-SEP-1996 p3NMF19.5 Mus musculus cDNA clone 331995

LOCUS W08345 299 bp DEFINITION mb41f02.rl Soares mouse

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l (bases 1 to 299)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                      Washid-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Enail: mouseset@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 YGGNTTYCCNTGGCCNGAYATGYTNGARTGYGAYMGNTTYCCNCARGAYAAYGAYTNTG
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Pred. No. 1.74e-227;
68; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                         The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                  Seg primer: mob.REGA+ET
High quality sequence stop: 280.
Location/Qualifiers
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larity 59.5%;
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Mus musculus
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es 175; Conser
                                                                                                                                            Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   human clone-49614 library-Soares infant brain INIB vector-Lafmid BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterata; Choanata; Tetrapoda; Anniota; Mammalia; Theria;
Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 231)
14 (bases 1 to 231)
15 (bases 1 to 231)
16 (bases 1 to 231)
17 (bases 1 to 231)
18 (bases 1 to 231)
19 (b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
WashU-Merck EST Project
WashU-Merck EST Project
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Enai: 314 286 1810
Enai: est@watson.wustl.edu
High quality sequence stops: 127
Source: IMAGE Consortium, LIANL
This clone is available royality free through LLNL; contact the IMAGE Consortium (info@inage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gagaccaagagcaagaccatttacaagctgaacggtgtgtccganag-gacctgaagaat 119|:|| ||:|| ||:|| ||:|| ||:||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1995
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    576 YGAYTTYGCNYTNAARATNAARGTNAARGARATNACNTAYATNAAYMGNGAYAC 629
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Pred. No. 4.01e-163;
51; Mismatches 51; Indels
                                                                                                                                                                           H29095 231 bp mRNA EST
Ym31e3.r1 Homo sapiens cDNA clone 49614 5'
H29095
9900005
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/clone="49614"
54 c 58 q 39
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Best Local Similarity 55.2%;
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
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                                                                                                                                                                                                                    DEFINITION
ACCESSION
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AUTHORS
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JOURNAL
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// Organization was mascaraed with a modified // Organization was prince 1: Not I; Site_2: Eco RI; Ist strand cDNA was prince with a Not I : oligo(dT) primer [5]; strand cDNA was primed with a Not I : oligo(dT) primer [5]; strand cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digsted with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
                                                                                                                                                                                                                                                                                                            Till (bases 1 to 250)

Marram., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Marram., Hillier,L., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

Unpublished (1996)
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  AA061047 250 bp mRNA EST 23-SEP-1996 mj78a12.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 482206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:292950
                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           699 RAARWSNGTNYTNTGGYTNAARGAYWSNYTNCARTGYACNTGYGARGARATGAAYGAYAT 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 gaaacggtggcagaagggccagagatagttcaagcgcatctcccgcagcatccgcaagct 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washur HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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/dev_stage="19.5 dpc total fetus"
/lab_host="pH10B (ampicillin resistant)"
<1..>250
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Pred. No. 5.97e-147;
48; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 179. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
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llarity 56.1%;
Conservative
                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                            house mouse.
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AA061047
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09-SEP-1996

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RESULT

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DEFINITION

ACCESSION

NID KEYWORDS SOURCE

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EST(expressed sequence tag).

EST(expressed sequence tag).

Caenorhabditis elegans (strain N2, ) (library: Yuji kohara unpublished cDNA) Hermaphrodite embryo embryo cDNA to mRNA.

Caenorhabditis elegans

Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;

Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditidae;

Rhabditidae; Caenorhabditis.

E 1 (bases 1 to 360)

S Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and Nishigaki,A.

Toward an expression map of the C.elegans genome

L Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                           Submitted (29-APR-1996) to the DDBJ/EMBL/GenBank databases. Yuji Kohara, Wational Institute of Genetics, Gene Library Lab; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp, Tel:0559-81-6854, Fax:0559-81-6855)
                                                                                                             EST(expressed sequence tag).

Caenorhabditis elegans (strain.N2) embryo hermaphrodite cDNA to mRNA, clone_lib:Yuji Kohara unpublished cDNA clone:yk173b2.

Caenorhabditis elegans

Bukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;

Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoldea;

Rhabditidae; Caenorhabditis.

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Kohara,Y., Motchashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome Unpublished (1996)
Location/Qualifiers
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C.elegans CDNA clone ykl17b4 : 5' end, single read.
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                                            end, single read.
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//strain="xx1"2"
//clone="yx1y1" Kohara unpublished CDNA"
//dev_stage="embryo"
//sex="hermaphrodite"
// sex="hermaphrodite"
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Pred. No. 1.49e-28;
29; Mismatches 71;
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       C.elegans cDNA clone ykl73b2
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Caenorhabditis elegans
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae.
1 (bases 1 to 531)
1 (bases 1 to 531)
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1 (bases 1, Durbin, R., Green, P., Shownkeen, R., Halloran, N., Hillier, L., Durbin, R., Berks, M., Du, Z., Thomas, K., Thlerry-Mieg, J.
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                                                                                         M89402 531 bp mRNA EST 02-DEC-1992 CELQBB2 Caenorhabditis elegans CDNA clone cm08b2 5' similar to frizzled protein precursor - Drosophila homologous peptide. M89402
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Box 8232,4566 Scott Ave., St. Louis, MI 63110, USA, or, Hills
Road, Cambridge CB2 204, UK

Road, Cambridge CB2 204, UK

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Fax: (USA) (314)3624137 or (UK) (0223)402008

Email: rw@nematode.wustl.edu or jes@mrc-lmb.cam.ac.uk.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Sulston, J.
A survey of expressed genes in Caenorhabditis elegans
Nature Genet. 1, 114-123 (1992)
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Pred. No. 2.81e-35;
46; Mismatches 151; Indels
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Best Local Similarity 37.5%;
Matches 118; Conservative
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Caenorhabditis elegans

Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;

Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditidae;

Rhabditidae; Caenorhabditis.

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C.elegans cDNA clone yk79d1 : 5' end, single read.
D74304
                                                                                                                                                                                                                       unpublished cDNA"
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Pred. No. 3.90e-23;
37; Mismatches 133; Indels
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Toward an expression map of the C.elegans genome Unpublished (1995)

Submitted (23-Aug-1995) to DDBJ by:
Yuji Kohara
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/strain="N2"
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/clone_lib="xuji kohara
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                                                                                                                                             /strain="N2"
/dev_stage="embryo"
/sex="Hermaphrodite"
                            Phone: 0559-81-6854
Fax: 0559-81-6855
Email:ykohara@ddbj.nig.ac.jp.
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Fax: 0559-81-6855
Email:ykohara@ddbj.nig.ac.jp.
Location/Qualifiers
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/sex="Hermaphrodite"
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National Institute of Genet.
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopteraygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 256)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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High quality sequence stops: 164
Source: IMAGE Consortium, LENL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (linfo@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                   106 ctatgcaaaggtattggctacaatatgacatcgctcccgaatagttatggacatgaaaa 165
                                                                                                                                                                                                                                                                                                                 166 caggaagaagccggattggaagttcatcaattttatccgctggtggaggtcggttgtttc 225
                                                                                                                                                                                                                                                                                                                                                                                                                226 caacatotoaaattottootetgoacaatgtacacocogatotgocaggaaaactacgac 285
                                                                                                                                                                                                                                              205 ATGAARGARGINYINGARCARGCNGGNGCNTGGAINCCNYINGINATGAARCARIGYCAY 264
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WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                       DB 89; Length 360
/tissue_type="embryo"
/clone_lib="Yuji kohara unpublished cDNA"
84 c 83 g 90 t 4 others
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                                                                                                                                           Pred. No. 5.43e-12;
32; Mismatches 105; Indels
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yo65b03.rl Homo saplens cDNA clone 182765 5'.
H45312
g921364
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/clone="182765"
70 c 79 g 4
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                                                                                                                    Query Match 5.6%;
Best Local Similarity 36.9%;
Matches 80; Conservative
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 206)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                  451 RRICRITRICYIGNGGRAANCKRICRCAYICNARCAIRICNGGCCANGGRAANCCRAANG 392
                                                                   134 agacgiccccitcgggaanciigicacacitaagcaictcgggccagtagaagccgaaga 193
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                                     Gaps
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Length 256;
 Score 40; DB 47; Length 256;
Pred. No. 4.79e-11;
15; Mismatches 25; Indels
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Pred. No. 2.72e-08;
16; Mismatches 31; Indels
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/clone="290113"
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Local Similarity 43.4%;
nes 36; Conservative
   Ouery Match 5.4%;
Best Local Similarity 49.4%;
Matches 39; Conservative
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AUTHORS
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Search completed: Tue Dec 9 09:33:30 1997 Job time : 1345 secs.

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m184a03.rl Stratagene (mm97f07.rl Stratagene (va52q08.rl Soares mou mb41f02.rl Soares mou 90h01.rl Beddington 1

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mr03c11.rl mr03c11.rl ze88f06.rl mh49d08.rl

AA122822 AA122822 AA082155 AA020088 AA023595 HS1147060

AA227473 AA044908 AA030216 G08492

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Match Mus. KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION REFERENCE AUTHORS RESULT 8 49:90ESTI 50:90EST2 51:90EST3 52:90EST4 53:90EST5 54:90EST5 56:90EST8 57:90EST9 58:90EST10 56:90EST10 61:90EST10 61:90EST10 61:90EST10 61:90EST10 61:90EST10 62:90EST11 60:90EST11 66:90EST10 63:90EST11 66:90EST10 65:90EST12 70:90EST21 70:90EST22 70:90EST21 70:90EST25 70:90EST21 70:90EST25 70:90EST21 70:90EST20 70:90EST21 70:90EST20 70:90EST21 70:90EST20 70:90EST21 70:90EST20 70:90EST21 70:90EST10 70:90EST20 70:90EST ......SNATNMGNAARYTNCARTGY 885 MasPar time 244.79 Seconds 993.543 Million cell updates/sec 1:EST109 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204 7:EST205 8:EST206 9:EST207 10:EST208 11:EST209 12:EST210 13:EST211 14:EST212 15:EST213 16:EST214 17:EST215 23:EST212 13:EST212 23:EST212 23:EST212 24:EST212 25:EST223 26:EST224 27:EST22 25:EST225 29:EST225 29:EST225 29:EST225 29:EST225 29:EST225 29:EST225 29:EST22 25:EST233 36:ST21 34:EST23 35:EST233 36:ST51 37:ST52 38:ST53 44:ST53 46:ST51 47:ST51 48:ST512 48:ST513 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. - n.a. database search, using Smith-Waterman algorithm Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc. Variance 4.699; scale 3.259 × 359085 seqs, 137405154 bases 1 ATGYTNCARGGNCCNGGNWS. TACRANGTYCCNGGNCCNSW. >848439-2-trans (1-885) from translate.seq Minimum Match 0% Listing first 45 summaries Tue Dec 9 09:33:55 1997; Dbase 0; Query 0 default EST-STS-THREE Mean 15.318; Tabular output not generated. EST-STS-FOUR TABLE Gap 6 n.a Post-processing: Title: Description: Perfect Score: N.A. Sequence: •• Scoring table: STD Statistics: Searched: Database: Database Nmatch Run on:

4.84e-216 6.95e-132 6.95e-132 7.52e-08 7.52e-02 7.52e-03 7.53e-03 7.5

G03067 AA144540 G27227 AA180957 AA009696 HSAA62672 AA122184 AA127092

37 56 12 10 89

mM80d03.ri Soares mou zr18a11.si Stratagene zf18a11.si Stratagene zf18a10.ri Soares mou human STS CHC. ATAllD D. melanogaster STS d mh06e01.ri Soares mou human STS MI-5108.mri 7712.ri Soares mou human STS SHGC-32136.zp41c03.ri Staraagene ze82h05.si Soares fet zs25f08.ri Soares NDH

DM57F11T AA013810 AA019228

zn28c08.s1 Stratagene 2q10e04.r1 Stratagene 4. human STS CHLC.GCT8C0 4. yv59d10.s1 Stratagene 4. zp69c10.s1 Stratagene 4. D. melanogaster STS d 2. mm45c07.r1 Soares mou 2. T1343 MVAT4 bloodstre 2. human STS BST186690. 2. 1353C3 czapPr605.1, p 2. ze71h06.s1 Soares fet 2. human STS MI-13950.

TB2692 AA019656

43 1

213 305 402 402

36 10 105

G09558 N53936 AA181149 DM52H6T

CKC0453.3prime Drosop yz30a03.sl Soares mul CpEST.119 pSKIIminusC CpEST.119 pSKIIminusC human STS SHGC-34074. mv26908.rl GuayWoodfo mv26908.rl GuayWoodfo z134f05.sl Soares pre

AA141629 N64746 AA224647 CPAA24647

443 24 62 80

AA241149 MM1157919 AA131693

1 (bases 1 to 458)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; AA105749 458 bp mRNA EST 04-FEB-1997 m184a03.r1 Stratagene mouse kidney (#937315) Mus musculus cDNA clone 518668 5' similar to TR:G1151260 G1151260 TRANSMEMBRANE RECEPTOR.;
AA105749 g1654838 Project The WashU-HHMI Mouse EST Unpublished (1996) Mus musculus house mouse. TITLE JOURNAL COMMENT

SUMMARIES

Query Result

Dubuque, T.,

848439-2-trans.rst2

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/strain="NIH/Swiss"
//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xhoi; Cloned unidirectionally. Primer: Oligo dr. 93
pooled NIH/Swiss 13 day embryo hearts. Average insert
Size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence:
GAATTCGCACGACTTTTTTTTTTTTTTTTT 3'"
/clone="536389"
                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/lab_host="SOLR (kanamycin resistant)"
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88; Mismatches 62;
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High quality sequence stop: 390.
Location/Qualifiers
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Fax: 314 286 1810
                                                       house mouse.
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                  AA073862 396 bp mRNA EST 15-FEB-1997 mm97£07.rl Stratagene mouse heart (#937316) Mus musculus cDNA clone 536389 5' similar to TR:G1151260 G1151260 TRANSMEMBRANE RECEPTOR.
                 Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 457.
Location/Qualifiers
1..458
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  Project
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Contact: Marra M/Mouse EST
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Best Local Similarity
Matches 280; Conserv
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                                                                ggacagaagcagggcgagctggtgatcacctccgtgaaacggtggcagaagggccag
                                                                                                                                               241 agagagttcaagcgcatctcccgcagcatccgcaagctgcaatgc 285
                                                                                                                                                                    Best Local Similarity
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Waterston R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished.
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W08345;
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    CNTGYAARAAYAARAAYGAYGAYAAYGAYATNATGGARACNYTNTGYAARAAYGAYT 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lln.gov) for further information. MGI:452086 Seq primer: -28ml3 rev2 ET from Amersham.
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                                                                                                                                                                                                           91896590
19-MAR-1997 (Rel. 51, Created)
19-MAR-1997 (Rel. 51, Last updated, Version 1)
va52908.rl Soares mouse 3NME12 5 Mus musculus CDNA clone 735038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished.
Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylle T., Lennon G., Soares B., Wilson
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Pred. No. 4.81e-249;
71; Mismatches 50; Indels 0;
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/lab_host="DH10B"
                                            tcgcactgaaaatcaaagtgaaggagataacgtacat 395
                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
"The WashU-HHMI Mouse EST Project";
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                                                                                                                                                                      standard; RNA; EST; 394
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larity 57.5%;
Conservative
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AA260087;
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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cg-cttcccctggccagacatgctggagtgcgaccgtttcccgcag-acaacgacctctg 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Mashington University School of MedicineP 4444 Forest Park Parkway, Email: At St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL: contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:213395 Seq primer: mob.REGA+ET High quality sequence stop: 280.
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ن
                                                                                                                                                                    CDNA clone 331995
                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson
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/clone_libe.Scares mouse p3NMF19.5"
/dev. stage="19.5 dpc total fetus"
/lab_host="DH10B (amplcillin resistant)"
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79 A; 95 C; 72 G; 53 T; 0 other;
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                                                                                          27-APR-1996 (Rel. 47, Created)
05-MAR-1997 (Rel. 51, Last updated, Version 2)
mb41f02.rl Soares mouse p3NMF19.5 Mus musculus
   ВР
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standard; RNA; EST; 299
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DEFINITION
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ORGANISM
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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/strain="C57BL6 x DBA"
/note="Vector: pGNW-SPORT; Site_1: Sall; Site_2: Notl;
/note="Vector: pGNM-SPORT; Site_1: Sall; Site_2: Notl;
/note="Vector: pGNM-SPORT; Site_1: Sall; Sa
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                 האסט 184 bp mRNA EST 29-JAN-1997 mo9901.rl Beddington mouse embryonic region Mus musculus cDNA AA209833
1808152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                             186 tgaagcctgcaaaaccaagaatgaggacgacaacgacatcatggaaacctttgtaaaaa 245
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396 YGGNTTYCCNTGGCCNGAYATGYINGARTGYGAYMGNTTYCCNCARGAYAAYGAYTNTG
                                                                                                                           catececetegetagtagegaceaecteetgeeggecacagaggaageteecaaggtgtg
                                                                                                                                                                                                                                                                                                                                     246 tgacttcgcactgaaaatcaaagtgaaggagataacgtacatcaacagagacac 299
                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Beddington mouse embryonic region"
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/dev_stage="7.5dpc"
/lab_host="DH128"
<1.>184
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Pred. No. 1.07e-135;
45; Mismatches 30;
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Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 147.
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Unpublished (1996)
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llarity 58.9%;
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Marra, M. Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marra, M., Hiller, L., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                            AA122822 523 bp mRNA EST 16-FEB-1997
mr03c11.rl Soares mouse 3NbMS Mus musculus cDNA clone 596372 5'.
AA122822
91681779
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                         120 cctgcagtgcacctgtgaggagatgaacgacatcaacgctccgtatctggtcatgggaca 179
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1 gataacgtacatcaacagagacaccaagatcatcctggagacaaagagcaagaccattta
                  /clone="596372"
/clone_lib="Soares mouse 3NbMS"
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High quality sequence stop: 469.
Location/Qualifiers
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Unpublished (1996)
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/dev_stage="4 weeks"
/lab_host="DH10B"
<1..>523
a 142 c 129 g 1
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                                                                                                                                                                                                                                                                                  AA122822 523 bp mRNA EST 21-NOV-1996
mr03c11.rl Soares mouse 3NbMS Mus musculus cDNA clone 596372 5'
AA122822
                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 469.
                                                                                                                                                           822 RMGNTGGCARAARGGNCARMGNGARTTYAARMGNATNWSNMGNWSNATNMGNAARYTNCA 881
                                                     1 tecgifycigitgaeteaaagaeageeigeagigeaeeigigaagaagaagaegaeateaae 60
                           Gaps
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                           ij
  Length 523;
                           Indels
Score 145; DB 56; I
Pred. No. 6.95e-132;
46; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares mouse 3NbMS"
/sex="male"
/dev_stage="4 weeks"
/lab_host="DH108"
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The WashU-HHMI Mouse EST Project
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larity 57.1%;
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les 105; Conser
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Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 48100
Fax: 314 286 48100
Fax: 314 286 1810
Email: est@vatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1171 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 262.
High quality sequence stop: 262.
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                                                                                                                            getecgtatetggteatgggaeagaageagggeggegageetggtgateacetecgtgaa 120
                                                                                                                                                                                                                                                                                                     121 acggtggcagaagggccagagagagttcaagcgcatctcccgcagcatccgcaagctgca 180
                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Lordata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 287)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Washl-Merck EST Project
Unpublished (1995)
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fetal heart NbHH19W Homo sapiens cDNA clone
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Length 523;
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/clone_lib="Soares fetal heart NbHH19W"
/sex="unknown"
Score 145; DB 6; Le
Pred. No. 6.95e-132;
46; Mismatches 32;
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Query Match 19.8%;
Best Local Similarity 57.1%;
Matches 105; Conservative
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                       713 GGYTNAARGAYWSNYTNCARTGYACNTGYGARGARATGAAYGAYATNAAYGCNCCNTAYY 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                        ij
                                                                                     Length 287;
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/lab_host="DH10B (ampicillin resistant)" <1..>287
                                                                                     Score 136; DB 32;
Pred. No. 1.67e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity on Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 444.
Location/Qualifiers
1..502
/organism="Mus musculus"
                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project Unpublished (1996)
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                                      8
2
                                                                                     Query Match 18.5%;
Best Local Similarity 58.6%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 502)
                                      84
C
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                    mRNA
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AUTHORS
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JOURNAL
COMMENT
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SOURCE

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LOCUS AA023595 213 bp mRNA EST 21-JAN-1997
DEFINITION mh80d03.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone 457253 5' similar to PIR:A45054 A45054 probable intercellular signal transducer or transmitter Fz-1;
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                       gggaacttctcgcacttgagtgtgtctggccactggaagccgaacttgttcatgagcgcc 158
                                                                                                                                                                                                                                                                                 377 GCRCANCKRICYTINACYIGNACRCANARNWSRI-GRCANGGYIGNAINGIYICRICNAR 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctgcaccttcaccagagggtagaactggtgcacctccagaccggcgtcctcctgattcgt 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 YIGYITCAINACNARNGGNAICCANGCNCCNGCYIGYICNARNACYICYITCAINGÍYIC 199
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                                                                                                                                                                                                     Gaps
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                                                                                                                                                    Length 502
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Possible reversed clone: similarity on
Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
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No;
/dev_stage="adult"
/lab_host="DH10B"
<1..>502
a 143 c 179 g
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                                                                                                                                                    Score
Pred.
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                                                                                                                                                 Query Match 7.5%;
Best Local Similarity 39.8%;
Matches 119; Conservative
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/clone="663740"
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AUTHORS
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JOURNAL
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   SEEEE
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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Econed into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exponentially growing neuroepithelial cells (Ntera-2/o1.D1). Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence:5' GAATTCGGGAGGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'"
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                                                                                                                                                                                                                                                                                                                                                                                                                              71 agcacaggaagagagcgcaggtccggtgagcagtggatctccacaagcggccagaattggt 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 geacetecaggeetgettegteetgegtgteatggttgaactggttgggeatgtgegtea 190
                                                                                                                                                                                                                                                                                                                                                                                       349 RNWSRIGRCANGGYIGNAINGTYICRICNARRICRICNARRCANACNGGNGCRAANARNW 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 CNGCYTGYTCNARNACYTCYTTCATNGTYTCRTGNCCNARNARRTTNGGNARNCKCATRT 170
                                                                                                                                                                                                                                                                                                                                                     11 gatggcggcacggtggtagcggcttgtggtagtcaggcaaacagatgggcgtgtacatag 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hiller L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Rucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; The WashU-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 SECANARRAAYTIYTINGTRICNGGRIGRCAYIGYTICATNACNARNGGNAICCANGCNC
                                                                                         /clone="457253"
/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 11
AA2147060 standard; RNA; EST; 421 BP.
AA227473;
g1849027
27-FEE-1997 (Rel. 51, Created)
27-FEE-1997 (Rel. 51, Last updated, Version 1)
zr18411.s1 Stratagene NI2 neuronal precursor 937230 Homo sapiens cDNA clone 663740 3'.
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                       Score 38; DB 28; Length 213;
Pred. No. 1.05e-08;
30; Mismatches 98; Indels
                                                                                                                                                                                                                   44
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                                                                                                                                                     /dev_stage="adult"
/lab_host="DH10B"
<1..>213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 ggttgtagccgatgcctcggca 212
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                                                                                                                                                                                                                                                                       Query Match 5.2%;
Best Local Similarity 36.6%;
Matches 74; Conservative
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xho1; Cloned unidirectionally. Primer: Oilgo dT.
Ninduced, exponentially growing neuroepithelial cells.
(Ntera-2/cl. Dl). Average insert size: 1.0 kb; Uni-ZaP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
/clone_1ib="Stratagene NT2 neuronal precursor 937230"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (Kanamycin resistant)"
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91849027
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Washu-Merck EST Project
Washu-Merck EST Project
Washu-Merck EST Project
Washu-Merck EST Project
4444 Forest Park Park Park Park Park
741: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. Er from Amersham
High quality: sequence stop: 225.
Location/Qualifiers
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/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                     308 aaataagagtggcagccataaggaatactatttataaaataaacagagttatagaggcta 367
                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 421)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Washuraston,R., Williamson,A., Wohldmann,P. and Wilson,R. Unpublished (1995)
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Pred. No. 7.52e-08;
16; Mismatches 31; Indels
                                                                               complement(<1..>421)
BP; 164 A; 55 C; 67 G; 135 T; 0 other;
                                                                                                                                                            Score 37; DB 82; I
Pred. No. 7.52e-08;
16; Mismatches 31;
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/organism="Homo sapiens"
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Best Local Similarity 43.4%;
Matches 36; Conservative
                                                                                                                                                                  5.0%;
                                                                                                                                                                                           Local Similarity 43.4%;
nes 36; Conservative
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707 TNYT 710
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Matches
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                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                           AUTHORS
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7el: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 887 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 314.
                                                               zf51e10.r1 Soares retina N2b4HR Homo sapiens cDNA clone 380490 5' AA044908 g1523130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            🔹 398 aaaatggtaagagaatgtcttagntactatgagttagggcnaaaattttttagatggggg 457
632 aratnatnytngaracnaarwsnaaracnatntayaarytnaayggngtnwsngarmgng 691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
<1..>512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="380490"
/clone_lib="Soares retina N2b4HR"
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                        368 ctttaaagaagaatgaactttgg 390
                                    692 AYYTNAARAARWSNGTNYINIGG 714
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/notes // /notes
                                                                                                                                                                                                                                               AA030216 432 bp mRNA EST 21-JAN-1997 mR87908.rl Soares mouse placenta 4NbMp13.5 14.5 Mus musculus cDNA clone 457982 5' similar to PIR:A45054 A45054 probable intercellular signal transducer or transmitter Fz-1;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l (bases 1 to 432)
Marrah... Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marrah... Hillier,L., Lacy,M., Le,M., Martin,J., Morris,M.
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE_Consortium (info@image.llnl.gov) for further information.
50 gcacacaggcgcgtacatggagcacaggaagtaacttgagctcggcg-gacactgcacctt 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 RCANACNGGNGCRAANARNWSRCANARRAAYTTYTTNGTRTCNGGRIGRCAYTGYTCAT 250
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Washugton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Local Similarity 38.8%; Pred. No. 3.49e-06;
es 66; Conservative 25; Mismatches 78
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
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/lab_host="DH10B"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Eukaryotae; I (bases 1 to 519)

S (coperative Human Linkage Center. Coperative Human Linkage Center. Unpublished (1955)

Synonyms: ATAIDIO, CHLC.ATAIIDIO.#T15621

GDB: GOO-364-870

Contact: Dr. Jeffrey C. Murray
Uof!

The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3308
Fax: (319) 356-3347
                                                                                                                                                                                                                                           STS sequence; primer; sequence tagged site.
human vector=pJCP1 host=E.coli dut+ung+ (DH10B) Marker Selected
genomic DNA prepared from XY individual of French nationality.
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109 caccagagggtagaactggtgcacctccagaccggcgtcctcctgattcgtgtggcccag 168
                               249 NACNARNGGNATCCANGCNCCNGCYTGYTCNARNACYTCYTTCATNGTYTCRTGNCCNAR 190
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Pred. No. 3.49e-06;
21; Mismatches 50; Indels 1; Gaps
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75 seconds at 55 degrees C
15 seconds at 72 degrees C
27 minutes at 72 degrees C
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each 1.5 pmole
each 200 uM
0.3 units
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/organism="Homo sapiens"
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Primer:
dNTPs:
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Total Vol:
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Primer B: TGTCCAGGAATATCACCACA
SIS size: 140
PCR Profile:
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KC1: 50mM
Tris: 10mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: jeff-murray@ulowa.edu
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Best Local Similarity 40.0%;
Matches 48; Conservative
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Search completed: Tue Dec 9 09:45:31 1997 Job time: 696 secs.

135:35 1997

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ILSLTWFLAAAMKWGNEAIAGYGQYFHLAAWLIPSVKSITALALSSVDGDPVAGICYV
GNQNLNSLRRFVLGPLVLYLLVGTLFLLAGFVSLFRIRSVIKQGGTKTDKLEKLMIRI
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MCLVVGIISGVWIWSGKTVESWRRFTSRCCCRPRRGHKSGGAMAAGDYPEASAALIGR
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                                                                                                                                                                                                             HSU43318 2334 bp mRNA PRI 24-FEB-1996
Human putative transmembrane receptor (frizzled 5) mRNA, complete
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Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2334) Wang,Y., Macke,J.P., Abella,B.S., Andreasson,K., Worley,P., Gilbert,D.J., Copeland,N.G., Jenkins,N.A. and Nathans,J. A large famility of putative transmembrane receptors homologous the product of the Drosophila tissue polarity gene frizzled J. Blol. Chem. 271 (8), 4468-4476 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205
Location/Qualiflers
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Pred. No. 5.31e-19;
0; Mismatches 117; Indels 0; Gaps
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Best Local Similarity 59.9%;
Matches 175; Conservative
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/translation="MEWGYLLEVTSLLAALAVLQRSSGAAASAKELACQEITVPLCK
GIGYNYTYMPNQFNHDTQDEAGLEVHQFWPLVEIQCSPDLKFFLCSMYTPICLEDYKK
PLPPCRSVCERAKAGCAPLMRQYGFAWPDRMRCDRLPEQGNPDTLCMDYNRTDLTTAA
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GGGAAPCEPGCQCRAPMYSYSSERHPLYNRVKTGQIANCALPCHNPFFSQDERAFTYF
WIGLMSVLCFVSTFATVSTFLIDMERFKYPERPIIFLSACYLEVSVGYLVRLVAGHEK
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SIAVLALSSVDGDPVAGICYVGNQSLDNLRGFVLAPLVIYLFIGTWFLLAGFVSLFRI
RSVIKQQGGPTKTHKLEKLMIRLGLFTVLYTYVPAAVVVACLFYEQHNRPFWEATHNCP
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                                                            619 agccgctgccgcctgccgctcggtgtgcgagcgcgccaaggccggctgctcgccgctga 678
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521 CGGACACCAAGAAGTTCCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACG 580
                                                                                                                     581 AGACCATCCAGCCATGCCACTCGCTCTGCGTGAGGTGAAGGACCGCTGCGCCCCGGTCA 640
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Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology an
Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street,
Baltimore, MD 21205
                                                                                                                                                                                    679 tgcgccagtacggcttcgcctggcccgagcgcatgagctgcgaccgcctccc 730
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Pred. No. 1.17e-17;
0; Mismatches 121; Indels
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/map="between Tpl2 and Cdh2"
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Vuong,V., Bambino,T., Liu,M.Y.C., Arnaud,C.D., Strewler,G.J. and
Nissenson,R.A.
                                                                                                                                                                                                                                                                                                                                   RATERZH 1912 DP MRNA ROD 16-JUL-1993 Rattus norvegigus Drosophila polarity gene (frizzled) homologue
                                                                                 515 GCCACCCGGACACCAAGAAGTTCCTGTGCTCTGTTTCGCCCCCGTCTGCCTCGAATGACC 574
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455 AGACCATGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGT 514
                                          getececeggaeetteaagtdetttetgtgtgtggdatgtdeaegeeeatetgeetggaggaet 485
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Rattus norvegicus (strain Sprague-Dawley) osteosarcoma cDNA
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J. Biol. Chem. 267, 25202-25207 (1992)
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/cell_line="UMR106-01"
/cell_type="osteoblast"
/tissue_type="osteosarcoma"
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zhao,z., Lee,C.C.' Baldini,A. and Caskey,C.T.
A human homologue of the Drosophila polarity gene frizzled has been
identified and mapped to 17q21.1
Genomics 27 (2), 370-373 (1995)

/organism-"Homo sapiens"

/clone\_lib="fz-2"

Location/Qualiflers 1..1923

96044450

JOURNAL MEDLINE

FEATURES

/tissue\_type="ovary"
/chromosome="17"

/map="17q21.1"

CDS

/gene="frizzled" /function="development"

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1923)

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HUMFRIZ 1923 bp mRNA PRI Human frizzled gene product mRNA, complete cds. L37882

rizzled gene; polarity gene

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Homo sapiens

ORGANISM

AUTHORS

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RDCAAPCEPARPDGSMFFSQEETRFARLMILTWSVLCCASTFFTVTTYLVDMQRFRYP ERPIIFLSGCYTMVSVAYIAGFVLQBRVVCNERFSEDGYRTVVOGTKREGCTILFMAL FFSMASSIWWYILSLTWFLAAGMKWGHEAIEANSQYFHLAAMAVPAVKTITILAAMGO IDGDLLSGVCHVGLNSTFRFYVLFIGTGFYLAAGFVLARTITILAAMGO KTEKLERLMYRIGGVSYLYVPATIVLACYFYLDFIGFSTLAGFVALRTIKHDGT KTEKLERLMYRIGGYSTLYTVPATIVLACYFYEQAAFRHWERSWVSGHCKSLAIPCPA HYTPPMASPDFTVYMIKYLMTLIVGITSGFWIMSGKTLHSWRKFYTRLINSRHGETTW" /translation="Mrprsalprillplilleragpaofhgekgisipdhgfcopisi plctdiaynotimpnilghtnoedaglevhofyplykvocspelrfflcsmrapvctv leqaippcrsicerarogcealmnkfgfqwperlrcehfprhgaeqicvgonhsedga PALLTTAPPPGLQPGAGGTPGGPGGGGAPPRYATLEHPFHCPRVLKVPSYLSYKFLGE 443 getgtgcacggacatcgcctacaaccagaccatcatgcccaaccttctgggccacacgaa 326 399 GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGAC 458 ccaggaggacgcaggcctagaggtgcaccagttctatccgctggtgaaggtgcagtgctc 386 CATGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCA 518 519 cccedacaccardargriccrerectectrecccccccccrerected 578 Gaps gooogaactgogottottootgtgotcoatgtacgcacccgtgtgcaccg-tg--ctgga э; Length 1923; Score 41; DB 80; Length 1923; Pred. No. 4.63e-08; 0; Mismatches 116; Indels /note="polarity gene; putative" /db\_xref="PID:g736679" 590 g 2.0%; ; ilarity 59.5%; i Conservative 671 c Best Local Similarity Matches 175; Conser Ø Query Match BASE COUNT ORIGIN 459 267 327 387 셤 à 셤 à 셤 ò

KFLGERDCAAPCEPARPDGSMFFSHHHTRFARLWILTWSVLCCASTFFTVTTSLVAMQ RFRYPERPIIFLSGCYTWVSVAXIAGFVLQERVVCNERFSEDGYRTVGGGTKKEGCTI LFMMLXFFSWASSIWWVILSLTWFLAAGMKWGHAAIEANSQYFHLAAWAVPAVKTITI

SEDGTPALLTTAPPSGLQPGAGGTPGGPGGGGAPPRYATLEHPFHCPRVLKVPSYLSY

LAMGQIDGDLLSGVCEVGLNRLDPLRGFVLAPLFVYLFIGTSFLLAGFVSLFRIRTIM KHDGTKTEPLERLMVRIGVFSVLYTVPATIVIACYFYEQAFREHWERSWYSQHCKSLA KHDGTKTEPLERLMVRIGVES/LXTVPALLY LACLE LEVEN COMMENTERTERLENSRHG IPCPAHYTPRTSPDETVYMIKYLMTLIVGITSGFWIWSGKTLHSWRKFYTRLTNSRHG

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/note="Drosophila polarity gene (frizzled) homologue

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Description:
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zd70e11.r1 Soares fet 0.00e+00
y374d07.r1 Homo sapie 0.00e+00
y128c05.r1 Homo sapie 0.00e+00
ze76g10.r1 Soares fet 0.00e+00
y128c05.r1 Homo sapie 2.91e-283
mb41f20.r1 Soares mou 1.30e-153
C.elegans CDNA clone 7.26e-25
F.C.elegans CDNA clone 7.26e-25
F.C.elegans CDNA clone 7.26e-25
F.C.elegans CDNA clone 7.26e-09
y276605.s1 Homo sapie 3.40e-13
y28801.s1 Homo sapie 2.64e-09
X276805.s1 Homo sapie 2.64e-09
R.C.elegans CDNA clone 7.26e-05
x976505.s1 Homo sapie 2.64e-09
X276605.s1 Homo sapie 2.64e-09
X276605.s1 Homo sapie 1.44e-05
x268b08.r1 Stratagene 1.14e-05
x276c08b08.r1 Stratagene 1.14e-05
x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.elegans CDNN clone 5.73e-04 wEST02441 Caenorhabdi 5.73e-04 yd62b09.rl Homo saple 5.73e-04 zb80a06.sl Soares sen 5.73e-04 zb87h03.sl Homo saple 5.73e-04 oll3m3 Plasmodium fal 3.77e-03
                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  179:EST179
184:EST184
189:EST189
194:EST194
6 177:EST177 178:EST178 1
182:EST182 183:EST183 18
187:EST187 188:EST188 1
1 192:EST192 193:EST193 1
6 197:EST197 198:EST198
                                                                    scale 3.547
                                                                                                                                                                      Description
                                                                    Variance 4.177;
                                                                                                                                                                                      74 W77968
78 AA073862
1 H87071
1 H16121
56 AA024771
1 H14917
1 H29095
1 H29095
1 AA061047
M89402
1 C09584
1 C09584
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HUM055B07B
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AA169546

NA169521

AA169521

W03474

W03474

HSC0EA112

AA027879

AA027879

AA027879

AA027879

AA027879

AA027879

AA027879

AA027870

AA027870

AA027870

AA027870

AA027870

AA02770

AA04436

AA04436

AA04436

AA0442770

AA04436

AA044236

AA044236

AA044236

AA044236

AA044236

AA044236
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R27662
CELK025G2R
T01720
T85962
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HSBA0B082
AA017479
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175:EST175 176:EST176 1
180:EST180 181:EST181 19
195:EST150 186:EST191 11
195:EST150 191:EST191 11
195:EST195 196:EST196 11
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N62714
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N98880
T09517
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bp mRNA EST 17-OCT-1996 fetal heart NbHH19W Homo sapiens cDNA clone

\* zd70e11.rl Soares fe 346028 5'. W77968 91388502 EST.

DEFINITION

RESULT LOCUS ACCESSION NID KEYWORDS clone

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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptco, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                           AA073862 396 bp mRNA EST 04-OCT-1996 mm97f07.rl Stratagene mouse heart (#937316) Mus musculus cDNA clo 536389 5' similar to TR:G1151260 G1151260 TRANSMEMBRANE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="NIH/Swiss"
//strain="NIH/Swiss"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. 93
pooled NIH/Swiss 13 day embryo hearts. Average insert
size: 1.0 kb; Unl.ZAP XR Vector; -5' adaptor sequence:
GAATTGGGCACAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTT 3'"
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousesetWastson.wustl.edu
This clone is available royalty.free through LLNL; contact the
                                                                                       587
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                  364 caagagcaagaccatttacaagctgaacggtgtccgaaagggaccttgaagaaatcgg
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Pred. No. 0.00e+00;
88; Mismatches 62;
                                                                                                                                                            647 TNYTNTGGYINAARGAYWSNYTNCARTGYACNTGYGARG 685
                                                                                                                                        424 tgctgtggctcaaagacagcttgcagtgcacctgtgaag 462
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Seq primer: primer name ambiguous
High quality sequence stop: 390.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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Best Local Similarity
Matches 245; Conserv
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Insert Length.1550 Std Error: 0.00
Seq primer: mbb.REGA+ET
High quality sequence stop: 424.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Parsons,J., Rifkin,L., Rohlfing,T., Le,M., Lennon,G., Marra,M., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                        Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108; Mismatches
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/dev_stage="19 weeks"
/lab_host="DH10B (amp
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holtman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
High quality sequence stops: 355
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                              179 tcccttggccagacatgctggagtgcgaccgtttccgcaggacaacgacctctgcatcc 238
                                                                                                                                    tectgtgetegetettegeeeetgtetgtetegaegaeetagatgagaeeateeageegt 119
                                                                                  gtcactcgctctg-gtgcaggtgaaggaccgctgcgccccggtcatgtccgccttcggct
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WashU-Merck EST Project
Washington University School of Medicine
4444 Encest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Homo sapiens
Eukaryotae; Metazoa; Bilateria; Coelomata; Osteichthyes; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopteryoii; Choanata; Tetrapoda; Ammlota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 406)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human clone=159560 library=Soares breast 3NbHBst vector=pT7T3D
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Y128c05.rl Homo sapiens cDNA clone 159560 5'
H16121
9880941
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Washu-Merck EST Project
Washington University School of Medicine
                                                                                                                      Score 304; DB 72;
Pred. No. 0.00e+00;
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/organism="Homo sapiens"
/clone="220525"
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128 c 110 g 83
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                                              High quality sequence stops: 321
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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heart NbHH19W Homo sapiens cDNA clone
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Vertebrata; Lo 414)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Parkway, Box 8501, St. Louis, MO 63108
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Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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09
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Pred. No. 0.00e+00;
89; Mismatches 60
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                                                                                                                     /organism="Homo sapiens"
/clone="159560"
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                                    Email: est@watson.wustl.edu
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Unpublished (1995)
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ze76g10.rl Soares fetal hr
34962.5'.
AA024771
g1489677
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Best Local Similarity 58.9%;
Matches 221; Conservative
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C
            Tel: 314 286 1800
Fax: 314 286 1810
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y126d03.rl Homo sapiens cDNA clone 159365 5' similar to SP.A45054
A45054 FZ-1-PUTATIVE INTERCELLULAR SIGNAL TRANSDUCER OR TRANSMITTER
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Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 288.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489
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/lab_host="DH10B (ampicillin resistant)"
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/clone_lib="Soares fetal heart NbHH19W"
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Pred. No. 0.00e+00;
85; Mismatches 54;
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larity 60.9%;
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Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrinii; Hominidae; Homo. 1 (bases 1 to 344)
Hiller, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Hordens, M., Waterston, R., Williamson, A., Wohldmann, P. and
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Soares mouse p3NMF19.5 Mus musculus cDNA clone 331995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
Emall: est@watson.wustl.edu
High quality sequence stops: 59
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Geisch,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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/clone_11b="331995"
/clone_11b="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                        Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Conteact: Wilson RK
WashUrMerck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 127
Source: IMAGE Consortium, Linni
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.lini.gov) for further information.
Location/Qualifiers
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Hillacr,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Tare,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                           17-JUL-1995
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516 YGAYTTYGCNYTNAARATNAARGTNAARGARATNACNTAYATNAAYMGNGAYAC 569
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Pred. No. 2.17e-170;
51; Mismatches 51; Indels
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54 c
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Best Local Similarity 55.2%;
Matches 128; Conservative
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1..250
/organism="Max musculus"
/organism="Max
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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AA061047 250 bp mRNA EST 23-SEP-1996 mj78a12.rI Soares mouse p3NMF19.5 Mus musculus cDNA clone 482206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@Image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gaaatccgtgctgtggctcaaagacagcctgcagtgcgcctgtgaggagatgaacat 60
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639 RAARWSNGTNYTNTGGYINAARGAYWSNYINCARTGYACNTGYGARGARARATGAAXGAYAT 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 1.30e-153;
48; Mismatches 34;
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Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 179.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
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Best Local Similarity 56.1%;
Matches 105; Conservative
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CDNA to

10

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DEFINITION

ACCESSION

KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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CELKI17B4F 360 bp mRNA EST 13-DEC-1995

Celegans cDNA clone ykl17b4 : 5' end, single read.

D76340

91122125

S EST (expressed sequence tag).

Canorhabditis elegans (strain N2, ) (library: Yuji kohara unpublished cDNA) Hermaphrodite embryo embryo cDNA to mRNA.

ISM Caenorhabditis elegans

ENAPORTORIA: Blagans

ENAPORTORIA: Rhabditia; Rhabditida; Rhabditina; Rhabditida; Rhabditida; Rhabditida; Caenorhabditis.

ENAPORTORIA: Tabara, H., Sugimoto, A., Watanabe, H. and Mishigaki, A.

Nishigaki, A.
C09584 360 bp mRNA EST 09-SEP-1996
SION C.elegans CDNA clone ykl73b2 : 5' end, single read.
C09584
G1534655
UDS EST(expressed sequence tag).
US EST(expressed sequence tag).
RNA, clone_lib:Yuji Kohara unpublished cDNA clone:ykl73b2.
VISM Caenorhabditis elegans
Extravotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
Secenorhabditis: Connorhabditis:
Secenorhabditis: Rhabditida; Rhabditina; Rhabditoidea;
Shabditidae; Caenorhabditis.
Sinians Rhabditina; Rhabditina; Rhabditoidea;
Secenorhabditis: Connorhabditis:
Sinians Rhabditina; Rhabditina; Rhabditoidea;
Sinians Rhabditians Rhabditians Rhabditina; Rhabditoidea;
Sinians Rhabditians Rhabditians Rhabditina; Rhabditoidea;
Sinians Rhabditians Rhabditians Rhabditina; Rhabditoidea;
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Submitted (29-APR-1996) to the DDBJ/EMBL/GenBank databases. Yuji
Kohara, National Institute of Genetics, Gene Library Lab; Yata
1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.]p,
Tel:0559-81-6854, Fax:0559-81-6855)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (sites)
Kohara,Y., Motchashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
Sano,M., Miyta,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organish...
/strain="N2"
/clone="yk173b2"
/clone_lib="Yuji Kohara unpublished cDNA"
/dev_stage="embryo"
/sex="hermaphrodite"
/sex="hermaphrodite"
/sex="hermaphrodite"
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Pred. No. 1.58e-30;
29; Mismatches 71
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Gene Library Lab.
National Institute of Genetics
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Local Similarity 41.9%;
les 72; Conservative
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SM caenorhabditis elegans Eunetazoa; Nematoda; Secernentea; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae.

I (bases 1 to 531)

I (bases 1 to 531)

Waterston, R., Martin, C., Craxton, M., Huynh, C., Coulson, A., Hiller, L., Durbin, R.K., Green, P., Shownkeen, R., Halloran, N., Hawkins, T., Wilson, R., Berks, M., Du, Z., Thomas, K., Thierry-Mieg, J., and Sulston, J.

A survey of expressed genes in Caenorhabditis elegans

L Nature Genet. 1, 114-123 (1992)
                                                                                                                                                                              gene
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Box 8232,4566 Scott Ave., St. Louis, MI 63110, USA, or, Hills
Road, Cambridge CB2 20H, WR
Fax: (USA) (314,3627072 or (UK) (0223)248011
Fax: (USA) (314,3624137 or (UK) (0223)402008
Email: rw@nematode.wustl.edu or jes@mrc-lmb.cam.ac.uk.
Location/Qualifiers
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123 c 136 g
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larity 37.5%;
Conservative
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Caenorhabditis elegans (strain N2, ) (library: Yuji kohara unpublished cDNA) Hermaphrodite embryo embryo cDNA to mRNA.

Caenorhabditis elegans

Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;

Eukaryotae; mitochondria! Rhabditida; Rhabditina; Rhabditidae;

Rhabditidae; Caenorhabditis.

1 (bases 1 to 360)

Lobars 1, Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and
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12 t 4 others
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Pred. No. 7.26e-25;
37; Mismatches 133; Indels
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/strain="N2"
/dev_stage="embryo"
/sex="Hermaphrodite"
                                                                                                             /organism="Caenorhabditis elegans"
                                                                                                                         /strain="N2"
/dev_stage="embryo"
/sex="Hermaphrodite"
/tissue_type="embryo"
/clone_lib="Yuji kohara ur
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C.elegans cDNA clone yk79d1 : 5'
D74304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institute of Genetics
Yata 1111, Mishima Shizuoka
                            Phone: 0559-81-6854
Fax: 0559-81-6855
Email:ykohara@ddbj.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 0559-81-6855
Email:ykohara@ddbj.nig.ac.jp.
Location/Qualifiers
Yata 1111, Mishima Shizuoka
411 Japan
                                                                                                                                                                                                                                                         Query Match 7.6%;
Best Local Similarity 36.8%;
Matches 99; Conservative
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1 (hases 1 to 256)
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                            106 ctatgcaaaggtattggctacaatatgacatcgctcccgaatagttatggacatgaaaa 165
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                         Length 360;
                a unpublished cDNA"
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Pred. No. 3.40e-13;
32; Mismatches 105; Indels
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/tissue_type="embryo"
/clone_lib="Yuji kohara
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The WashU-Merck EST Project
Unpublished (1995)
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Homo sapiens
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Best Local Similarity 36.9%;
Matches 80; Conservative
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopterygil; Choanata; Terrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 206)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifklin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Fax: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 161
Source: InAGE Consortium, Lini
This clone is available royalty-free through Lini; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                  01-MAR-1996
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WashD-Merck EST Project
WashIngton University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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   Length 256;
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Pred. No. 2.64e-09;
16; Mismatches 31; Indels
Score 40; DB 47; Length 256
Pred. No. 3.35e-12;
15; Mismatches 25; Indels
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 Query Match 5.8%;
Best Local Similarity 49.4%;
Matches 39; Conservative
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Best Local Similarity 43.4%;
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Search completed: Tue Dec 9 10:38:56 1997 Job time : 1366 secs. 848439-3-trans.rst2

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Release Copyrigh	e 2.1D John F. Collins, Biocomputing Research Unit. ght (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a. Run on: Tabular output no	<ul> <li>n.a. database search, using Smith-Waterman algorithm</li> <li>Tue Dec 9 10:39:19 1997; MasPar time 224.95 Seconds</li> <li>ot generated.</li> </ul>
Title: Description: Perfect Score: N.A. Sequence: Comp:	>848439-3-trans (1-825) from translate.seq 688 1 WSNGCNMGNGGNYINTTYYTSNATNMGNAARYTNCARTGY 825 SWNCGNKCNCCNRANAARRAWNTANKCNTTYRANGIYACR
Scoring table:	TABLE default Gap 6
Nmatch STD :	Dbase 0; Query 0
Searched:	359085 seqs, 137405154 bases x 2
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	EST-STS-THREE  1:EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204 7:EST205 8:EST200 3:EST201 0:EST209 11:EST209 12:EST201 13:EST201 14:EST212 15:EST213 16:EST214 17:EST215 18:EST21 14:EST212 15:EST213 16:EST214 17:EST215 23:EST212 44:EST22 25:EST223 26:EST224 27:EST225 23:EST22 25:EST22 36:EST228 31:EST23 33:EST230 33:EST231 34:EST223 35:EST233 36:STS1 37:STS2 38:STS3 33:EST24 40:STS5 41:STS6 42:STS7 43:STS8 44:STS9 45:STS10
Database:	S415-14 4 7.515-12 49 9.90-15-14 50 9.90-15-14 50 9.90-15-14 50 9.90-15-14 50 9.90-15-14 70 9.90-15-
Statistics:	Mean 14.890; Variance 4.327; scale 3.441

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query

Result

Description Pred. No.	49 m184a03.rl Stratagene 0.00e+00 62 mm97f07.rl Stratagene 0.00e+00	1087 va52g08.rl Soares mou 7.48e-mb41f02.rl Soares mou 6.10e-2	3 mogOhOl.rl Beddington 6.64e-14	22 mr03c11.rl Soares mou 7.24e-14	ze88f06.rl Soares fet 8.23e-12	18 mh49d08.rl Soares mou 1.99e-2	of sileall.sl Stratagene 4.29e-0	3 zrl8all.sl Stratagene 4.29e-0	8 ZISLETU.rl Soures ret 3.44e=0 6 mh87a08 rl Soures mon 2.66e-0	human STS CHLC.ATA11D 2.66e-0	T D. melanogaster STS d 1.97e-0 n mb06e01 r1 somres mon 1 97e-0	ze59c03.rl Soares ret 1.41e-0	human STS WI-5108. 1.41e-0	.0 mri/iiz.ri soares mou 1.41e-0 72 zs23f08.rl soares NbH 6.23e-0	human STS CHLC.GCT8C0 6.23e-0	] D, melanogaster STS d 3.85e-0 32 mh45a07.rl Soures mou 3.85e-0	.6 mh45c07.rl Soares mou 3.85e-0	6 ze61f11.s1 Soares ret 3.85e-0	1353C3 czapPFDd2.1, D 3.85e-0	0 ze71h06.sl Soares fet 3.85e-0	human STS WI-13950. 3.85e-0	<pre>cku2453.3prime Drosop 3.85e-0 vz30a03.s1 Soares mul 3.85e-0</pre>	37 CpEST.119 pSKIIminusC 3.85e-0	7 CpEST.119 pSKIIminusC 3.85e-0	119 mv26q08.rl GuayWoodfo 3.85e-0	9 mv26g08.rl GuayWoodfo 3.85e-0	IT D. melanogaster STS d 2.26e-0	22538 Lambda-PRL2 Ara 2.26e-0	00 mr19c02.rl Soares mou 2.26e-0	numan sis chic.AIAISC 2.206-0	8807 mr18b06.rl Scares mou	SING	mRNA EST 04-FEB-1997 use kidney (#937315) Mus musculus cDNA to TR:G1151260 G1151260 TRANSMERANE				. eukaryotes; Metazoa; Chordata; lentia; Sciurognathi; Muridae; Murinae;		s,M., Dietrich,N., Martin,J., Morris	an, F., Underwood, K., Moore G., Soares, B., Wilson, R.	Project	
ch Length DB ID	.9 458 33 A	.2 394 101 .5 299 94	.5 184 20	.1 523 56	.8 287 32	.0 502 21	.4 421 82	4 421 63	1 432 29	519 39	.9 288 36	.8 241 21	.8 252 37	.5 407 89	.5 451 39	4 177 36	.4 213 10	.4 305 21	.4 402 1	.4 407 21	.4 425 43	4 435 34	.4 455 80	.4 455 62	.4 503 92	.4 503 70	.2 170 36	.2 367 75	.2 386 56	2 42/39	5 CJ C		. 458 bp r1 Stratagene mo 8668 5' similar	 φ. α.		mouse.	; mitochondrial; Eutheria; Roc	1 to 458)	Hillier, L., Kucaba, T.,	rg,K., Stept 1., Wylie,T.,	R. HHMI Mouse EST	id (19
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/strain="C57/B16"
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                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:312516
Seq primer: -28ml3 revl ET from Amersham
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 0.00e+00;
103; Mismatches 75; Indels
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AA073862

ACCESSION

DEFINITION

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1 (bases 1 to 396)
Marta, M., Hiller, L., Allen, M., Bowles, M., Districh, N., Dubuque, T.,
Marta, M., Hiller, L., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theislang, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                    Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      through one round of normalization, and was constructed by Bento Somres and M. Fatima Bonaldo."
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Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project MashIngton University School of MedicineP 4444 Forest Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information. MGI:452086 Seq primer: -28ml3 rev2 ET from Amersham.
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Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
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19-MAR-1997 (Rel. 51, Last updated, Version 1)
va52g08.rl Soares mouse 3NME12 5 Mus musculus cDNA clone 735038
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 7.48e-265;
71; Mismatches 50; Indels 0;
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Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr
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cg-cttcccctggccagacatgctggagtgcgaccgtttcccgcag-acaacgacctctg 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:213395 Seq Finded: mob.REGA+ET High quality sequence stop: 280.
                                                                            ggacagaagcagggcgacggctggtgatcacctccgtgaaacggtggcagaagggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ж,
                                                                                                                                                                                                                                                                                                                                                                                  27-APR-1996 (Rel. 47, Created)
05-MAR-1997 (Rel. 51, Last updated, Version 2)
mD41f02.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 331995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/clone="331995"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
<1..>299
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                                                                                                                                                                    241 agagagttcaagcgcatctcccgcagcatccgcaagctgcaatgc 285
                                                                                                                                                                                               79 A; 95 C; 72 G; 53 T; 0 other;
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Pred. No. 6.10e-230;
68; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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llarity 59.5%;
Conservative
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schallenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL6 x DBA"
/note="Vector: pcMv-SPORT; Site_1: Sall; Site_2: Notl;
Cloned unidirectionally. Primer: Oligo dT. Gastrulating
embryos were collected at 7.5dpc from C57BL6 x DBA
matings, excluding embryos that had developed head folds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and all extraembryonic tissues. Average insert size: 1.3 kb (range: 0.5 - 3.0 kb). Referenced in Development 121, 2479-2489 (1995)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                     mosolol.rl Beddington mouse embryonic region Mus musculus cDNA AA209833 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
336 YGGNTTYCCNTGGCCNGAYATGYTNGARTGYGAYMGNTTYCCNCARGAYAAYGAYYTNTG 395
                                                                         396 YAINCCNYINGCNWSNWSNGAYCAYINYINCCNGCNACNGARGARGARGARGINIG 455
                                                                                                                                  tgaagcctgcaaaaccaagaatgaggacgacaacgacatcatggaaaccctttgtaaaaa 245
                                                                                                                                                      catcoccctcgctagtagcgaccacctcctgccggccacagaggaagctcccaaggtgtg
                                                                                                                                                                                                             246 tgacttcgcactgaaaatcaaagtgaaggagataacgtacatcaacagagacac 299
                                                                                                                                                                                                                                 /clone_lib="Beddington mouse embryonic region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seg primer: -28ml3 revl ET from Amersham
High quality sequence stop: 147.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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/dev_stage="7.5dpc"
/lab_host="DH125"
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Best Local Similarity 58.9%;
Matches 109; Conservative
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AUTHORS
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45; Mismatches 30; Indels

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1 (bases 1 to 523)
Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through Hento Founds of normalization, and was constructed by Pento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                               AA122822 523 bp mRNA EST 16-FEB-1997
mr03c11.r1 Soares mouse 3NDMS Mus musculus cDNA clone 596372 5/
91681779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                   1 gataacgtacatcaacagagacaccaagatcatcctggagacaaagagcaagaccattta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares mouse 3NbMS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 469.
Location/Qualifiers
1..523
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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/dev_stage="4 weeks"
/lab_host="DH10B"
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                    мал 22822 523 bp mRNA EST 21-NOV-1996
mr03c11.rl Soares mouse 3NbMS Mus musculus cDNA clone 596372 5'
AA122822
g1681779
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Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                            Gaps
                                                   1 tccgtgctgtggctcaaagacagcctgcagtgcacctgtgaggagatgaacgacatcaac
                                                                                                                                                     acggtggcagaagggccagagagagttcaagcgcatcccgcagcatccgcaagctgca
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
 Length 523;
                            Indels
  Score 145; DB 56; I
Pred. No. 7.24e-141;
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                            46; Mismatches
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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Seq primer: -28M13 rev2 from Ame
High quality sequence stop: 469
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21.18;
larity 57.18;
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               Similarity
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   Query Match
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BASE COUNT
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Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1171 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 262.
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                                                                                                                                                                    gotocgtatotggtcatgggacagaagcagggcggcgagcctggtgatcacctccgtgaa 120
                                                                                                                                                                                            121 acggtggcagaagggccagagagagttcaagcgcatctcccgcagcatccgcaagctgca 180
                                                                                                                                                                                                                                                                              Homo sapiens

Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;

Eutheria; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 287)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,

Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp mRNA EST 01-FEB-1997 fetal heart NbHH19W Homo sapiens cDNA clone
                                             Gaps
                                             ;;
  Length 523;
                                           Indels
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/clone_lib="Soares fetal heart NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
Score 145; DB 6; Le
Pred. No. 7.24e-141;
46; Mismatches 32;
21.1%;
ilarity 57.1%;
Conservative
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g1624408
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schallenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                               653 GGYTNAARGAYWSNYTNCARTGYACNTGYGARGARATGAAYGAYATNAAYGCNCCNTAYY 712
                                                                                                                                                                                                                                              tggtcatgggacagaaacagggtggggagctggtgatcacctcggtgaagcggtggcaga 120
                                                                                                                                                                   ggctcaaagacagcttgcagtgcacctgtgaggagatgacgacatcaacgcgccctatc 60
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                constructed by Bento Soares and M.Fatima Bonaldo." /clone="445839" /clone_lib="Soares mouse placenta 4NbMpl3.5 14.5" /sex="unknown"
                                                                                                                                                                                                                                                                                                                                          aggggcagagagttcaagcgcatctnccggnngnatccgcaagctgcagtgc 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                              Indels 1;
                                                                                              Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possible reversed clone: similarity on wrong strand
Seq primer: -28Mi3 rev2 from Amersham
High quality sequence stop: 444.
_iocation/Qualifiers
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                              41; Mismatches 30;
                                                                                            Score 136; DB 32;
Pred. No. 8.23e-129;
                                      51 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project Unpublished (1996)
                                        δ
                                      82
                                                                                          Query Match 19.8%;
Best Local Similarity 58.6%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 502)
                                      84 C
                     <1..>287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
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                                    COUNT
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AUTHORS
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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LOCUS AA023595 213 bp mRNA EST 21-JAN-1997
DEFINITION mh80d03.rl Scares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone 457253 5' similar to PIR:A45054 A45054 probable intercellular signal transducer or transmitter Fz-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 213)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                        218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                    gggaacttctcgcacttgagtgtgtctggccactggaagccgaacttgttcatgagcgcc 158
                                                                                                                                                                                                                                                                                                                   377 GGRAANCKRICRCAYICNARCAIRICNGGCCANGGRAANCCRAANGCNWSCAINACNGGN 318
                                                                                                                                                                                                                                                                                                                                                                                                                            317 GCRCANCKRICYTINACYIGNACRCANARNWSRI-GRCANGGYIGNAINGIYICRICNAR 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 -t-a-cggtgcacacaggcgcgtacatggagcacaggaagaacttgagctcggcgtacga 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 ctgcaccttcaccagagggtagaactggtgcacctccagaccggcgtcctcctgattcgt 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 YTGYTTCATNACNARNGGNATCCANGCNCCNGCYTGYTCNARNACYTCYTTCATNGTYTC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 giggcccagcaggitgggcaigatggictggitgiacgcgaigtccgigcacagcggga 394
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                        159 tegeagecetggegtgegegetegeacageggageggeagggeggtaegeetgegteeag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                     Length 502;
                                                                                                                                                                                                            44; Mismatches 132; Indels
                                                                                                                                                  Score 55; DB 21;
Pred. No. 1.99e-27;
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                                                                          102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Mus musculus"
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/dev_stage="adult"
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             /lab_host="DH10B"
<1..>502
                                                                                                                                                           8.0%;
39.8%;
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
                                                                          143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                        Query Match
Best Local Similarity
Matches 119; Conserv
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Zr18a11.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 663740 3'.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 225.
Location/Qualifiers
     /clone="663740"
/clone_lib="% tratagene NT2 neuronal precursor 937230"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="Soln Knamycin resistant)"
complement(<1..>421)
BP; 164 A; 55 C; 67 G; 135 T; 0 other;
                                                                                                                                                                                                                    308 aaataagagtggcagccataaggaatactatttataaaaataacagagttatagaggcta 367
                                                                                                                                                                                                                                                         572 ARATNATNYINGARACNAARWSNAARACNAINTAYAARYIINAAYGGNGTNWSNGARMGNG 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Stratagene NT2 neuronal precursor 937230"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 aaataagagtggcagccataaggaatactatttataaaataaacagagttatagaggcta 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dukaryotze:

Vertebrata; Eutheria; Primates; Catarrhin; Honinidae; Homo.

1 (bases I to 421)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,N.,

Rolman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.

Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,

Washu-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, NO 63108
                                                                                                                                          Length 421;
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                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 63; Length 421
Pred. No. 4.29e-09;
16; Mismatches 31; Indels
                                                                                                                                                                               16; Mismatches 31;
                                                                                                                                          Score 37; DB 82;
Pred. No. 4.29e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                              368 ctttaaagaagaatgaactttgg 390
                                                                                                                                                                                                                                                                                                                                   632 AYYTNAARAARWSNGTNYTNTGG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="663740"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
WashU-Merck EST Project
                                                                                                                                          5.4%;
larity 43.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 43.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 285 1810
                                                                                                                                                           Local Similarity
nes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                     Sequence 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
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Matches
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I 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally, Primer: Oligo dT. Uninduced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exponentially growing neuroepithelial cells (Ntera-2/c1.D1). Average insert size: 1.0 kb; Uni-2AP XR Vector: -5' adaptor sequence:5' GAATTCGGAGGAG 3' -3' adaptor sequence: 5' CTCGAGITTTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                              71 agcacaggaagaagcgcaggtccggtgagcagtggatctccacaagcggccagaattggt 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 SRCANARRAAYITYTINGTRICNGGRIGRCAYIGYITICAINACNARNGGNAICCANGCNC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 gcacctccaggcctgcttcgtcctgcgtgtatatggttgaactggttgggcatgtgcgtca 190
                                                                                                                                                                                                                                                                                                                                                    gatggcggcacggtggtagcggcttgtggtagtcaggcaaacagatgggcgtgtacatag 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through Linl.; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 225.
                                                                                                                    /clone_lib="Soares mouse placenta 4NbMP13.5 14.5" /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-1997 (Rel. 51, Created)
27-FEB-1997 (Rel. 51, Last updated, Version 1)
27-FEB-1997 (Stratagene NT2 neuronal precursor 937230 Homo sapiens CDNA clone 663740 3'
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                          Length 213;
                                                                                                                                                                                                                                                                                                                   98;
                                                                                                                                                                                                                                                                              Score 38; DB 28; Pred. No. 5.16e-10;
                                                                                                                                                                                                                                                                                                                 30; Mismatches
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Key Location/Qualifiers
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HS1147060 standard; RNA; EST; 421
AA227473;
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                                                                                                                                                         /dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 TYTGRIAYTCNAINCCRIGRCA 88
                                                                                                                                                                                                                                                                              36.68;
                                                                                                                                                                                                                    51 c
                                                                                                                                                                                                                                                                                                                   74; Conservative
                                                                                                                                                                                                    <1..>213
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/strain="C57BL/6J
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                                                                                                                                                                                                                                                                                         Mus musculus
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Matches 66; Conser
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JOURNAL
COMMENT
                                                                                                                                                                                                                         ACCESSION
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0
                                                                                                                                    AAO44908 512 bp mRNA BST 02-FEB-1997 zf51e10.rl Scares retina N2b4HR Homo sapiens CDNA clone 380490 5' similar to contains L1.t2 Ll repetitive element ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enail: est@watson.wustl.edu
This clone is available royalty free through LLNL ; contact the
TMAGE Consortium (info@mage.llnl.gov) for further information.
Insert Length: 887 Std Error: 0.00
Seq primer: -28MI3 rev2 from Amersham
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                                                                                                                                                                                                                                                Eucaryotae: mitochondrial eukaryotes; Metazoa; Chordata; Eukaryotae: Eutheria; Primates; Catarrhini; Hominidae; Homo.

Vertebrata: Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Cases I to 512)

Hiller, C., Clark, M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. WashU-Merck EST Project
   572 aratnatnytngaracnaarwsnaaracnatntayaarytnaayggngtnwsngarmgng 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK Washd Medicine Washd Merck EST Project Washngton University School of Medicine 4444 Parks Parkway, Box 8501, St. Louis, NO 63108 Tel: 314 286 1800 Fax: 314 286 1810
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Pred. No. 3.44e-08;
20; Mismatches 57; Indels
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/lab_host="DH10B (ampicillin resistant)"
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/clone="380490"
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Location/Qualifiers
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                                                            AYTUNARRANKUSUGUNTENTGG 654
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Best Local Similarity 37.9%;
Matches 47; Conservative
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AUTHORS
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AA030216 432 bp mRNA EST 21-JAN-1997 mh87g08.rl Soares mouse placenta 4NbMpl3.5 14.5 Mus musculus cDNA clone 457982 5' similar to PIR:A45054 A45054 probable intercellular signal transducer or transmitter Fz-1;
                                                                                                                                                                                                                                                                                                     (bases 1 to 432)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Rogels,X., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
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                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 goacacaggogogtacatggagoacaggaagaagttgagottggggg-gacactgcactt 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 399.
Location/Qualifiers
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Pred. No. 2.66e-07;
25; Mismatches 78;
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/organism="Mus musculus"
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/lab_host="DH10B"
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human STS CHLC.ATAllD10.P16004 clone ATAllD10.

N G08492

STS GHC.ATAllD10.P16004 clone ATAllD10.

STS Sequence: primer; sequence tagged site.

human vector-pJCPl host-E.Coli dut+ung+ (DH10B) Marker Selected penomic DNA prepared from XX individual of French nationality.

Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 519)

Murray,J., Sheffield V, Weber,J.L., Duyk,G. and Buetow,K.H.

Cooperative Human Linkage Center

Unpublished (1995)

Synonyms: ATAllD10, CHLC.ATAllD10.#T15621

GDB: GOO-364-870

Contact: Dr. Jeffrey C. Murray

Uofi
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109 caccagaggtagaactggtgcacctccagaccggcgtcctcctgattcgtgtggcccag 168
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Pred. No. 2.66e-07;
21; Mismatches 50; Indels 1;
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75 seconds at 55 degrees C
15 seconds at 72 degrees C
27
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                                                                                                                                            The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Department of Pediatrics, Iowa City, IA 52242, USA
Department of Pediatrics, Iowa City, IA 52242, USA
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu
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each 200 uM
0.3 units
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/organism-"Homo sapiens"
14..153
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Primer B: TGTCCAGGAATATCACCACA
STS size: 140
PCR Profile:
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complement(134..153)
a 87 c 93 g
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KCl: 50mM
Tris: 10mM
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Search completed: Tue Dec 9 10:48:48 1997 Job time: 569 secs.

GAATTCGGCCTTCATGGCCT.......AAAAAAAAAAAAGGGCGGC 2027 CTTAAGCCGGAAGTACCGGA......TTTTTTTTTTTTCGCCGGCG 18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7 25:BCT8 62:BCT9 27:BCT1 0 28:BCT11 29:GEN1 30:GEN3 31:GEN3 32:HTG1 33:HTG2 34:HTG3 35:INV1 36:INV2 37:INV3 31:GEN3 32:HTG1 33:HTG2 34:HTG3 35:INV1 36:INV2 37:INV3 38:INV4 39:INV5 40:INV6 41:INV7 42:INV9 44:INV1 44:INV1 46:MAM1 47:MAM2 48:MAM3 49:VTT1 50:VRT2 51:VRT3 52:VRT4 53:PAT1 54:PAT2 55:PAT4 56:PAT4 57:PAT5 58:PHG 59:PLN1 60:PLN3 61:PLN3 62:PLN4 63:PLN4 63:PLN4 65:PLN7 66:PLN8 67:PLN8 67:PLN8 67:PLN8 67:PLN8 67:PLN8 67:PLN8 67:PLN8 67:PLN8 67:PRN1 73:PRN1 77:PRN 77:PR MasPar time 1674.10 Seconds 1329.789 Million cell updates/sec (ME) embl-new3 1:BCT 2:FUN 3:GENI 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC n.a. - n.a. database search, using Smith-Waterman algorithm Release 2.1D John F. Collins, Blocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc. 106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV 112:MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRI2 118:ROD 119:SYN 120:UNA 121:VRL U-emb150\_99 Variance 6.329; scale 1.942 362067 seqs, 549138275 bases x >US-08-848-439-1 (1-2027) from US08848439.seq 2027 summaries Tue Dec 9 07:57:40 1997; Dbase 0; Query 0 Minimum Match 0% Listing first 45 default Mean 12.293; genbank-new3 Tabular output not generated. 17:VIR genbank99 TABLE Gap 6 Gap Post-processing: Title: Description: Perfect Score: .. Scoring table: Sequence: STD Statistics: Comp: MPsrch\_nn Searched: Database Database Database Mmatch Run on: N.A.

Shirozu, M. 101777, Direct Submission Bobs/EMBL/GenBank databases. Michio Submitted (01-MAY-1995) to the DDBJ/EMBL/GenBank databases. Michio Shirozu, Kyoto University, Faculty of Medicine, Department of Medical Chemistry; Yoshida, Sakyo-ku, Kyoto, Kyoto 606, Japan (E-mail:kondo@vituus].virus.kyoto-u.ac.jp, Tel:81-75-753-4387, 2 (bases 1 to 1776) Rattus norvegicus Dro 1.59e-10
Human filzzled gene p 4.63e-08
Sequence 5 from paten 7.33e-07
Sequence 5 from paten 2.40e-02
Oxytricha fallax 57kD 8.07e-02
A.thaliana hsc70-1 ge 8.07e-02
Caenorhabdiis elegan 2.40e-02
Oxytricha fallax 57kD 8.46e-01
Oxytricha fallax 57kD 8.46e-01 Mus musculus cell\_line:ST-2 cDNA to mRNA, clone\_lib:phage (lgt22a) library, ST-2 directional 1. Mus musculus 4 66 e - 01 4 66 3.46e-01 2.63e+00 2.63e+00 46e-01 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 19-DEC-1996 10g (a) on to Human placental antic Sequence 3 from paten Sequence 3 from paten M.musculus VAC-alpha Human mRNA for vascul Human blood coagulati Sequence 2 from paten R.filosa mRNA for alp H.sapiens PP4 mRNA. Escherichia coli from
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REFERENCE

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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455 t
                                            proteins
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Shirozu, M., Tada, H., Tashiro, K., Nakamura, T., Lopez, N.D.,
Nazarea, M., Hamada, T., Sato, T., Nakano, T. and Honjo, T.
Characterization of novel secreted and membrane proteins isolated
Genomics 37 (3), 273-280 (1996)
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Hamada,T., Tada,H., Nakamura,T., Nelson,L.D., Martina,N., Hamada,T., Sato,T., Tashiro,K., Nakano,T. and Honjo,T. Isolation of novel genes encoding for escreted or membrane using signal sequence trap (Dpublished (1995)
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/db_xref="PID:g1151252"
/translation="MARPDPSAPPSLLLLLAQUVGRAAAASKAPVCQEITVPMCRGI
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PRCBYCERARAGCSPLMAQYOFAWPBENSCORLEVLGREDSTUCMDYNRSEATTAPP
RPFRAKPTLPGPPGAPASGGECPAGCPFVCKGREPFVPILKESHPLYNKYRTGOYPNC
AVPCYQPSFSADERTFAIFWIGLMSVLCFISTSTTVATFLIDMDTFRYPBRPITFLSA
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ILSLTWFLAAAMKWGNEAIAGYGQYFHLAAWLIPSVKSITALALSSVDGDPVAGICYV
GNQNLNSLRRFVLGPLVLYLLVGTLFLLAGFVSLFRIRSVIKQGGTKTDKLEKLMIRI
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MCLVVGITSGVWIWSGKTVESWRFTSRCCCRPRRGHKSGGAMAAGDYPEASAALTGR
TGPPGPAATYHKQVSLSHV"
                                                                                                                                                                                        HSU43318 2334 bp mRNA PRI 24-FEB-1996
Human putative transmembrane receptor (frizzled 5) mRNA, complete
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Mang, Y., Macke, J.P., Abella, B.S., Andreasson, K., Worley, P., Gilbert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J. A large family of putative transmembrane receptors homologous the product of the Drosophila tissue polarity gene frizzled J. Biol. Chem. 271 (8), 4468-4476 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 2334)
Abella, B., Wang, Y., Macke, J.P. and Nathans, J.
Direct Submission
Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205
Location/Qualifiers
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                                                                                              1959 AAACATTATATTCTT-GTATATAAACTTT 1986
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/gene="frizzled
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/translation="m
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WIGLWSVLFCVSTFATVSTLLDMERFKYPEREI FILSAGVLFVSVGYLTVRLVAGHEK
WACSGGAPGAGGRGGAAAAGGAGAAGRGASSPGARGEYEELGAVEGHYRYETTGPA
LCTVVFLLVYFFGMASSIWWYILSLTWFLAAGMKWGNEAIAGYSGYFHLAAWLVPSVK
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CLRDLQPDQARRPDYAVFMLKYFMCLVVGITSGVWVWSGKTLESWRALCTRCCWASKG
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Vertebrata, Eutheria, Rodentia, Sciurognathi, Myomorpha, Muridae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMU43321 2421 bp DNA ROD 24-FEB-1996
Mus musculus putative transmembrane receptor (frizzled 8) gene,
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                                                                                                                                                              306 tgccgttgtgcaaaggcatcggttacaactacattadatgcccaaccaggttgaaccacg 365
521 CGGACACCAAGAAGTICCIGIGCICGCICTICGCCCCCGICIGCCICGAIGACCIAGACG 580
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Abella, B., Wang, Y., Macke, J.P. and Nathans, J.

Direct Submission
Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205
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                                                                                                                                                                                                                                                                                              Score 56; DB 87; Length 2421;
Pred. No. 1.17e-17;
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/note="putative transmembrane receptor"
/codon_start=1
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RTITILAGGVDGGGCYPPHPPMSPDFTVFMIKYLMPLACFFERDWSGWGFFSKNAQ
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                          (frizzled) homologue"
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459 CATGAAGGAGGTGCTGGAGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCA
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Pred. No. 2.40e-02;
82; Mismatches 95; Indels
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0; Mismatches 107; Indels
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                        /note="Drosophila polarity gene
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Patent: US 5569830-A 5 29-0CT-1996;
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5 from patent US 5569830.
                                                                                                                                                                                                                                                                                                                                                                                     Score 38;
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1..215
/organism="unknown"
a 8 c 25 g
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1255 c 1220 q
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Local Similarity 61.6%;
hes 181; Conservative
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Local Similarity 11.0%;
les 22; Conservative
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Unclassified.
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KEYWORDS
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinee, Rattus.
1 (bases 1 to 4540)
Chan, S.D.H., Karpf, D.B., Fowlkes, M.E., Hooks, M., Bradley, M.S., Vuong, V., Bambino, T., Liu, M.Y.C., Arnaud, C.D., Strewler, G.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATFRZZH 4540 bp mRNA ROD 16-JUL-1993
Rattus norvegicus Drosophila polarity gene (frizzled) homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Two homologs of the Drosophila polarity gene frizzled (fz) are widely expressed in mammalian tissues J. Biol. Chem. 267, 25202-25207 (1992)
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579 GAGACCATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGT 638
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Rattus norvegicus (strain Sprague-Dawley) osteosarcoma cDNA
                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 215)
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                      Score 39; DB 57; Length 215;
Pred. No. 7.33e-07;
72; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 others
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                                                                                                                                                      128278 215 bp DNA
Sequence 5 from patent US 5569830.
128278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Sprague-Dawley"
/cell_line="UMR106-01"
/cell_type="osteoblast"
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8 c 25 q
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Best Local Similarity 14.7%;
Matches 24; Conservative
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/translation="HTRDLXKHLLKAHKKXXEXEXXXXXLKXLXKRKAREXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-FEB-1997) to the EMBL/GenBank/DDBJ databases. Oncological Science, University of Utah, School of Med. Rm5C334,
                                                                        13-MAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein chimera gene, partial
                                                                                                                                                                                                                                     MEDIINE; 94134747.

Doak T.G., Doerder F.P., Jahn C.L., Herrick G.;

A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common 'D35E' motif";

Proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
                                                                                                                                                                                                                                                                                                                                                                            Witherspoon D.J., Doak T.G., Williams K., Seger J., Herrick G "Selection on the protein-coding genes of the TBE1 family of transposable elements in the ciliates Oxytricha fallax and O.
                                                                                                                                               Oxytricha fallax
Eukaryotae; mitochondrial eukaryotes; Alveolata; Ciliophora;
hypotrichs; Stichotrichida; Oxytrichidae; Oxytricha.
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A.thaliana hsc70-1 gene.
X77199
g450879
heat shock cognate 70-1; hsc70 gene.
thale cress.
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/db_xref="PID:g1881676"
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standard; DNA; INV; 354
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Best Local Similarity 25.0%;
Matches 22; Conservative
                             g1881675
13-MAR-1997 (Rel. 51,
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USA, UT 84132, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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QAXEXXXVXXXRNXLXSEXTKIMIKIQYKKIPVLAQIDLDTSLQSYLILEDSFDKKVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="this is a bulk sequence that was generated from PCR product that represents many transposon templates"
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Oxytricha fallax 57kD zinc finger/protein chimera gene, partial
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                       124 ktamtsrnrtgktannavdsrnmgdasvgsdkntkkhaknsadgkvgsknngdrnnrygt 183
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Eukaryotae; Alveolata; Ciliophora;
hypotrichs; Stichotrichida; Oxytricha.

1 (bases 1 to 34)
Doak,T.G., Doerder,F.P., Jahn,C.L. and Herrick,G.
A proposed superfamily of transposase genes; transposon-like elements in ciliated protozoa and a common 'D35E' motif Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
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Witherspoon.D.J., Doak,T.G., Williams,K., Seger,J. and Herr:
Witherspoon.D.J. protein-coding genes of the TBE1 family of
transposable elements in the ciliates Oxytricha fallax and (
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Doak,T.G., Williams,K., Witherspoon,D.J. and Herrick,G.Direct Submission
Submitted (11-FEB-1997) Oncological Science, University School of Med. Rm5C334, USA, UT 84132, USA
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/db_xref="PID:g1881676"
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Pred. No. 8.07e-02;
37; Mismatches 29; Indels
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/codon_start=1
                                                                                                                                                     184 gtksnvsnncgggnkrdvss 203
                                                                                                                                                                                        561 CTGCCTCGATGACCTAGACG 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="9D1
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Best Local Similarity 25.0%;
Matches 22; Conservative
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KNQVAMSPWIVTPARRLIGRRESDSSVQSDWKLMPEKIQAGPADKFWIYVEYKGEBK
EFAAELISSWLIKMREIAAYLGVTIKNAVYTVPAYFNDSQRQATRDAGVIAGLNVM
RIINEPTAAAIAYGLIKKATRVGEKNVLIFDLGGGTFPVSLLTIEEGIFEVKATAGDT
HLGGEDFDNRAVNHFVQEFKRSKKDITGNPRALRRLRTSCERAKRTLSSTAQTTIEI
DSLYEGIDFYSTITRARFEELMMDLFRKCMEPVEKCLRDAKKNESTYHDVYLVGGSTR
IPKVQQLLQDFNGKELCKSINPVEAVVGAAVQGALLGGEGNEKVQDLLLLDVTPLS
IGGLEFAGGVWTYLIPPKKEQVFSTYSDNQPGYLLQYFGEBRATKDNNLLGR
FELSGIPPAARGVPQITVCFDIDANGILNVSAEDKTTGQKNKVTITNDKGRLSKDEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAGKGKGPAIGIDLGTTYSCVGVWQHDRVEIIANDQGNRTTPSY
VAFTDSERLIGDAAKNQVANNPVNTVFDAKRLIGRRFSDASVQSDRQLWPFTII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KMVQEAEKYKSEDEEHKKKVEAKNALENYAYNMRNTIQDEKIGEKLPAADKKKIEDSI
EQAIQWLEGNQLAEADEFEDKMKELESICNPIIAKMYQGAGGEAGGPGASGMDDDAPP
                                                                                                                                                         Direct Submission
Submitted (22-JaN-1994) K. King, Dept of Genetics, Universitaet
Tuebingen, Auf der Morgenstelle 28, 72076 Tuebingen, FRG
Location/Qualiflers
Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
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Pred. No. 8.07e-02;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                join(<1.171,496..2238)
/gene="Hsc70-1"
/codon_start=1
/product="heat shock_cognate 70-1"
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/db_xref="PID:9450881"
/db_xref="SWISS-PROT:P22954"
                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/strain="Ostweerfalen"
/tissue_type="leaf"
/clone="Athsc70g"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="PID:9450880"
/db_xref="SWISS-PROT:P22953"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(3695..3908,4217..>4297)
/gene="Hsc70-2"
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/note="see also M23106"
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/gene="Hsc70-2"
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/gene="Hsc70-2"
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                                                                                                                       (bases 1 to 4297)
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Caenorhabditis elegans

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Caenorhabditis Rhabditida; Rhabditina; Rhabditoidea;

Rhabditidae; Caenorhabditis.

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Rhabditidae; Caenorhabditis.

El (Rases It on 3826.)

Miscon, R., Alnascough, R., Anderson, K., Baynes, C., Berks, M.,

Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,

Coulson, A., Craxton, M., Dear, S., Durbin, R., Favello, A.,

Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,

Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,

Latreille, P., Lighthing, J., Lloyd, C., McMurray, A., Mortimore, B.,

Sunders, D., Shownkeen, R., Smaldon, N., Smitth, A., Sonnhammer, Staden, R., Sulston, J., Thierry Mieg, J., Thomas, K., Vaudin, M.,

Waughan, K., Waterston, R., Watson, A., Weinstock, L.,

Wilkinson-Sproat, J. and Wohldman, P.,

2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The 5' cosmid is C07D10, 200 bp overlap;3' cosmid is T19C12. Actual start of this cosmid is at base position 197 of CELK02A2; actual end is at bp 38262 of CELK02A2
2021 GCTTTTTTTTTTTTTTTAGGTAAAACAGGATGTAAAGTTTATATACAAGAATATAATG 1962
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Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
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3384...3656,3705...3804,4217...4404)
/gene="K02A2.2"
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                                                                                              3042 tttatctggatttttactttgacgttttatgctttattt 3081
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                                                                                                                                  Caenorhabditis elegans cosmid K02A2. U23171
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Submitted by:
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Hallsworth, K.
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INLDFTETSFTESLFDDFYRSGTPNEDLEGAMKLNIHKMNTSYRLNRYIRENSPDSQL
ILNLPSPSPRNRLAFNNSYMTYLDVLTEDLPRVLFIGGSGREVITIDS"
join (26353..26567,26616..26712,26757..26894,28725..29289,29341..29441)
/gene="K02A2.1"
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/db_xref="PID:9726385"
/tb_xref="PID:9726385"
/translation="MSDRSNYSNRFVSYVNAYFHFFLVAGLTFQCILLYLIRTKSPAS
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FLGVTFCVALSISNYVIYRFLILRRRDITKKHLIYIIILSYYPGIITTYAPLILISFN
LVSVFLTDEVTFYFEKLSKLLAQEHGYVALVTDIYGKGIRCTDISSAVTLLRPMTSDR
                                                                                                                             CESAYHFELGVALCVGLGISNTIIFRPQALRKGRVSRSRIFTMISLTYIPSSITIVYL
NYFLRIKNNLTMISQILPFTSSWDFEKVRSLTYIEHPKYDLSIYEPFVGFHNIASFQF
TLATLLLVIGAYAIPAISGFLTSRVIHLINDNRGMSLKTKEQSKTLAYGLACQTFLPV
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/db_xref="PID:9726384"
/translation="MLSDDFSLFSYDYDDKADAHDADAAFRKFEALCSARSQQPSTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref-"PID:g726386"
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ASSFISGYTTPGPKERATSEUVKANLGVVLPTIQHILGVTWFIRLFWVGMSGY
AWTMALLAICCLSTLLTSISLSAVANNGVNESGGAYFIISRNLGAEFGSAGTLEYLA
NTVAASWYIVGGVEVILMYLMPEMAIGGADALHDTEMFGSLYNNLRLYGTVFLLIQAL
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FTDPESAGIAPSGVGYDANAEKRSWKATLEFIKEAFA"
complement(join(29971..30119,30168..30403,30450..30655))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MADDSNRFVLYFDVYYYSYFIIGVFAQSVLIYLKNKSPPRLYS
FCYFLINTWIVQFAVLLMTFFTQSRCLPNSTTYTVLPRGPCKYFGPTACFAGYHISLA
VSMAVALSFANTVLFRYLPIRFHGFNKNLFFDDDNCMLHSSNISCDCTFSGHLGFSKS
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complement(join(33175..33695,33825..35082,35609..37636))

gone="K02A2.6"

/note="similar to silkwork transposon mag (PIR:S08405) and POL polyprotein (reverse transcriptase)"
                                                                                                                                                                                                     ICYIPVASCYIFSOMTSVELLLNEHLLGILICFPSFVDPFISFYFIVPYRQALLGLFK
CRWTRRLNIVIVINHLSKRNPSIVDSN"
complement(join(4846..4918,4971..5077))
/gene="K02A5.2"
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KNNEPFLGLVLTVIIAECGIILGAVDKIAEVLDFFFIMTLSLLGAALCFFIMFASSVP
LACIACTATAVIYKYVEWKGAKKEWGDGMRGLALTTAQYSLLKVEDKDPHPKNWRPQV
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TLVROMSSVRLRGFAKTWFYNNHQINGTISGIZQSIGGERPRTILLMWPURRDE
LVLFBEETIHGANDVCLIVYRGIIDFPEYSBRLTGFDIWWTVQDGILMLIAYLLR
QHKVWKGCTIRIFAVSEQDSTKSEDMRAGLQKYIYMLRIDAELFIVDLLDMEVSDEVV
                                                                          /db_xref="PID:9726382"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVAMGVKFVQLLAPVSLMCVILAIAACIGGGIEKQITMEGMKVCAIDNHLLQSSIVTH
PIKNOTSWFRETVDFCULCKGLYLESYFCANVNDBASAEDDVFCTHYTSKRYTCQ
LAFPGFNMKTLNDNMAPEYMEKSEVPGFKGFTAEVVQDESSTFFMLAAIYFPRVTG
IFTGTNMSGDLRDPQRSIPVGTIAATLITSAIYYILAILFGGSITRSVLRDKFGRSIG
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20735..21024,21067..21346,21423..21621,21674..21793,
21924..22110,22353..22900,22950..23072,23118..23551,
23600..23743,23809..23993,24055..24070))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to bumetanide-sensitive Na-K-C1 cotransporter (PIR:A53491)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein E04F6.1"
/note="similar to C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence-not_experimental
                                                        /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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CDS

CDS

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VNOVSTSETSAKIEVMLKNDFPEVEKGGLGTKEREMEFRTEENAPVPKRARPVPY
GSLEAVETELNRLOGEMGY VYPTIYAKWAAPIVYKKKGTGKIRVCABFKCSGLAMALK
GSLEAVETELNRLOGEMGY VYPTIYAKWAAPIVYKKKGTGKIRVCABFKCSGLAMALK
DEFHPLPTSEDIFSRLKGTVYSQIDLKDAYLQVELDEEAQKLAVINTHRGIFKYLRMT
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VEASFKKNEKLKLSSYDDFSWAFFIDMHQQSKIVSVRVPTNRSKKK
KPIPRKPEKSSQDSKKKGEIPPCFYCNKGHTANDRSNFRFGKGCSSV
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VEHPSTSTGTPRGSTSTQLGQASTRNGSRYTASGRNPSCQGNRYSSIRGEGVTARRER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein chimera gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Doak T.G., Doerder F.P., Jahn C.L., Herrick G.;

A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common 'D35E' motif";

Proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
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hypotrichs; Stichotrichida; Oxytrichidae; Oxytricha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 37; Length 382
Pred. No. 2.40e-02;
0; Mismatches 18; Indels
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13-MAR-1997 (Rel. 51, Last unde
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|larity 73.1%;
|Conservative
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,; (7)

Gaps .; 7

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U01687:44..120,U01688:110..203,U01689:38..133,
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/gene
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Fernandez, M.P., Morgan, R.O., Fernandez, M.P., Morgan, R.O., Fernandez, M.P., Morgan, R.O., Fernandez, M.R. and Carcedo, M.T. The gene encoding human annexin V has a TATA-less promoter with Gene 149 (2), 253-260 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSANX5S11 565 bp DNA PRI 10-JAN-1997
Human annexin V (ANX5) gene, exon 13 and 3'-untranslated region.
9430964
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       product that represents many transposon templates'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 aaagaaargcdagrgaryhhyhdwargwbgydgwgc-yykaayaagcwagmgarwyaswr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | | : :| :| :: :::|: :: :| | | ::|| | :|| | | :|| | | :|| | | :|| | | :|| | | :|| | | :|| | | :|| | | :|| | | :|| | | :|| | | :|| | | :|| | | :|| | | :|| | | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | 
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Submitted (14-SEP-1993) Fernandez M.P., Universidad de
Departamento de Biología Funcional, c/Julian Claveria,
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 111; Length 354; Pred. No. 8.46e-01;
                                                                          /codon_start=1
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/db_xref="PID:g1881676"
                                                                                                                                                                                                                                                                                                                      111 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49; Mismatches 51; Indels
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1..565
/organism="Homo sapiens"
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Matches 42; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AXEXXXVXXXRNXLXSEXTKIMIKIQYKKIPVLAQIDLDTSLQSYLILEDSFDKKVIX
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2 (bases 1 to 354)
Witherspoon, D.J., Doak, T.G., Williams, K., Seger, J. and Herrick, G. Selection on the protein-coding genes of the TBE1 family of transposable elements in the ciliates Oxytricha fallax and O.
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3 (bases 1 to 354)
3 (bases 1 to 354)
Doak,T.G., Willhams,K., Witherspoon,D.J. and Herrick,G.
Direct Submission
Submitted (11-FEB-1997) Oncological Science, University of Utah,
School of Med. Rm5C334, USA, UT 84132, USA
Location/Qualifiers
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Science, University of Utah, School of Med. Rm5C334,
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1.4%; Score 28; DB 8; Length 354;
Best Local Similarity 29.2%; Pred. No. 8.46e-01;
Matches 42; Conservative 49; Mismatches 51; Indels
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Best Local Similarity 80.4%; Pred. No. 8.46e-01;
Matches 37; Conservative 0; Mismatches 9; Indels
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Search completed: Tue Dec 9 08:36:17 1997 Job time: 2317 secs.

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SUMMARIES

Description Pred N	Mouse SDF5 mRNA, comp 0.00e+0 Mus musculus putative 5.75e-2 Human putative transm 2.82e-1 Caenorhabditis elegan 3.27e-1 Mus musculus putative 9.21e-1 Drosophila melanogast 7.21e-1	Mus musculus putative 5.54e-10 Caenorhabditis elegan 1.13e-08 Rattus norvegicus bro 1.13e-08 Human frizzled gene p 8.23e-08 Rattus norvegicus bro 5.83e-07 Caenorhabditis elegan 5.83e-07 Caenorhabditis elegan 5.83e-07	Caenorhabditis elegan 5 83e-0 Sequence 5 from paten 1.05e-05 Sequence 5 from paten 6.91e-05 Mus musculus frizzled 1.76e-04 Oxytricha fallax 57kp 1.10e-03	Oxytricha fallax 57kD 3.89e- Oxytricha fallax 57kD 3.89e-0 Human DNA sequence ** 9.24e-0 Insertion sequence IS 5.03e-0 Mycoplasma hyorhinis 5.03e-0 Insertion sequence IS 5.03e-0 H Plasmodium falciparum 5.03e-0 Mycomodium falciparum 5.03e-0	Mus muscutus pucar Muman DNA sequence Xenopus laevis Frz Xenopus laevis Frz M.hyorhinis vipA. Caenorhabditis ele *** SEQUENCING IN Periplaneta fuligi	Dictyostelium discoid 5.79e+0 Caenorhabditis elegan 5.79e+0 1 Yeast crminNl gene fo 5.79e+0 Ceratitis capitata yo 5.79e+0 Mouse dystrophin mRNA 5.79e+0 Caenorhabditis elegan 5.79e+0	Human Xp22 cosmid Ú25 5.79e+0 Caenorhabditis elegan 5.79e+0 Caenorhabditis elegan 5.79e+0 X O.sinensis chloroplas 5.79e+0 TS	mRNA ROD 19-DEC-1996 ete cds.	e:ST-2 cDNA to mRNA, clone_lib:phage (lgt22a) onal 1. rial eukaryotes; Metazoa; Chordata; Rodentia; Sciurognathi; Muridae; Murinae;	) to the DDBJ/EMBL/GenBank databases. Michio ity, Faculty of Medicine, Department of hida, Sakyo-ku, Kyoto, Kyoto 606, Japan irus.kyoto-u.ac.jp, Tel:81-75-753-4377,
gth DB	776 85 421 87 334 77 770 38 831 87 085 40	60 87 113 38 23 80 12 90 76 38	4576 111 215 57 215 57 2624 87 354 8 354 111	354 111 354 8 911 33 509 23 513 24 518 23 187 43	491 07 571 34 2291 11 2875 52 284 24 745 33 413 44	1054 39 3618 38 4413 69 7698 35 3815 88 6321 35	731 78 569 37 874 38 704 63	1776 bp 5 mRNA, comp.	lus cell_lin ST-2 directi. lus e; mitochond a; Eutheria;	M. ubmission ubmission Kyoto Univer Chemistry; Yo Kyoto Gooyiusi; Kondooyiuusi; S-753-4388)
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Shirozu, M., Tada, H., Tashiro, K., Nakamura, T., Lopez, N.D.,
Nazarea, M., Hamada, T., Sato, T., Nakano, T. and Honjo, T.
Characterization of novel secreted and membrane proteins isolated
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                                                                   REFERENCE
AUTHORS
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     AUTHORS
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                                                       JOURNAL
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/codon_start=1
/codon_start=1
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PLPPCRSVCRRAKAGCAPLMRGYGENWPDRMRCDRLPEGGNPDTLCMDYNNTDLTTAA
PSPPRRLPPPPPPGGAPLMRGYGENWPDRMRCDRLPEGGNPDTLCMDYNTDLTTAA
PSPPRRLPPPPPPPGGAPLMRGYGENWPDRMSCGSGNAAAPPSRGGKARPP
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                                                                                    793
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1 (bases 1 to 2421)
Wang,Y., Mack-J.P., Abella,B.S., Andreasson,K., Worley,P.,
Gilbert,D.J., Copeland, N.G., Jenkins,N.A. and Nathans,J.
A large family of putative transmembrane receptors homologous
the product of the Drosophila tissue polarity gene frizzled
J. Biol. Chem. 271 (8), 4468-4476 (1996)
atttacaagctgaacggcgtgtccgaaagggacctgaagaaatccgtgctgtggctcaaa 733
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                       ggacagaagcaggcggcgactggtgatcacctccgtgaaacggtggcagaagggccag
                                                                                        gacagcctgcagtgcacctgtgaggagatgaacgacatcaacgctccgtatctggtcatg
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Pred. No. 5.75e-24;
47; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="frizzled 8"
/note="putative transmembrane receptor"
                                                                                                                                                                                                                                                                   2 (bases 1 to 2421)
Abella, B., Wang, Y., Macke, J.P. and Nathans, J.
Direct Submission
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188..2245
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/organism="Mus musculus"
/chromosome="18"
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Pred. No.
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Best Local Similarity 41.1%;
Matches 124; Conservative
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                       Query Match 10.9%;
Best Local Similarity 39.7%;
Matches 116; Conservative
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AUTHORS
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GYNLTHMPNQFNHDTODEAGLEVHQFWRLVETQCSPDLRFFLCTMYFFTCLPPYHKPL
PPCRSVCERAKAGGSPLAMPGRAFERMSCDRLPVLGRDAEVLCMDYNRSEATTAPP
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AVDCYQPSFSANDERTPATFWIGLMSVLCFISTSTVANFLIDMDTFRYPERPILELSA
CYLOCYGPEFSANDERTPATFWIGLMSVLCFISTSTVANFLIDMDTFRYPERPILELSA
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MCLVVGITSGVWLWSGKTVESWRRAALTCACROHDTGQPRAKFEXWLMLKYF
TGPPGPAATYHKQVSLSHV"
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Human putative transmembrane receptor (frizzled 5) mRNA, complete
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                                         486 acaagaagcetetgcegeettgtegetetgtgtgtgaacgegecaaggeeggetgegege 545
                                                                                                                                                                                                                                                                         260 TNGAYGARACNATNCARCCNTGYCAYWSNYTNTGYGTNCARGTNAARGAYMGNTGYGCNC 319
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                                                                                                                                  140 ARACNATGAARGARGINYINGARCARGCNGGNGCNTGGAINCCNYINGINATGAARCART 199
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Wang X., Macke, J.P., Abella, B.S., Andreasson, K., Worley, P., Gilbert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J. A large family of putative transmembrane receptors homologous the product of the Drosophila tissue polarity gene frizzled J. Blol. Chem. 271 (8), 4468-4476 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205
                                                                                                                                                                                                                                                                                                                               cgctcatgcgccagtacggctttgcttggcctgaccgcatgcgctgcgatcggttgccgg
                   tgccgttgtgcaaaggcatcggttacaactacacttacatgcccaaccagttcaaccacg
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Abella, B., Wang, Y., Macke, J.P. and Nathans, J.
Direct Submission
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/organism="Homo sapiens"
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321..2078
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/map="2q33-34"
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AUTHORS
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CEU43316 1770 bp DNA INV 24-FEB-1996 Caenorhabditis elegans putative transmembrane receptor (frizzled 1) 99ne, complete cds.
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SCIDYTHHLLFVVGGLSHYPCSSVASLIYYTATCSRLWMLLICVSRNKATRTSHL
DDSRTRVIMLILGIPLAPLMALLARAVAANPLITGLFFIGAASPGTDWIFNFCRELIL
FLISSIALSSACRLLGSDEODVYGFAGYTAAVYPLAGLFYMLSFVNDATQPFLSLDR
SFNAVSATKFSFDLLLSFINCAFCLIYLLFKLITRSSSKVSKEGYQPAVPRLPPQPAIPG
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PNLVDESSWASSESITYPLLSVVCSEQLKFFLCSVYFPMCNEKLANPIGFCRPLC
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SEDDGNDRVEDIQREVDRLNGKCPQDEVFLNRSSKCVPLCSNPQKVGGTDRESATRLL
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;

Eukaryotae, mitochondrial eukaryotes; Metazoa; Nematoda;

Enernentea; Rhabditia; Rhabditia; Rhabditina; Rhabditidae;

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I (bases 1 to 1770)

Manoj, Y., Macke, J.P., Abella, B.S., Andreasson, K., Worley, P.,

Gilbert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J.

A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled
J. Biol. Chem. 271 (8), 4468-4476 (1996)
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                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agccgctgccgcctgccgctcggtgtgcgagcgcgccaaggccggctgctcgccgctga
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                                                                                         Score 75; DB 77; Lei
Pred. No. 2.82e-17;
44; Mismatches 132;
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/fb_xref="PID:g1151254"

/franslation="MAWPGGTPBSSRGAPGGVGIRLGLLLGFLLLLRPTLGFGDEBERR

CDFTRIAMCONLGFYTKMPMLVGHELQTDAELQLTTFTPLIGYGCSSQLQFFLCSVY

VPMCTEKINIPIGPCGGMCLSVKRRCEPVLREFGFAMPDILNCSKFPPONDHNHMCME
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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1 (bases 1 to 2831)

Wang, Y., Macke, J.P., Abella, B.S., Andreasson, K., Worley, P., Gibbert, D.J., Copeland, M.G., Jenkins, N.A. and Nathans, J. A large family of putative transmembrane receptors homologous the product of the Drosophila tissue polarity gene frizzled J. Blol. Chem. 271 (8), 4468-4476 (1996)
                                                                                                                                                                   77 AYYTNCARYTNTGYCAYGGNATNGARTAYCARAAYATGMGNYTNCCNAAYYTNYTNGGNC 136
                                                                                                                                                                                                    264
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                                                                                                  Gaps
                                                                                                                                                                                                    aggaatcatggaaagacgcctccgaatccatcctcacctacaagcccctgctctccgttg
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                                                               Length 1770;
                                                               Score 64; DB 38; Length 177
Pred. No. 3.27e-12;
47; Mismatches 150; Indels
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               493
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SVRSNTYASTFRINNMI"
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                                                                 Query Match 9.3%;
Best Local Similarity 37.5%;
Matches 118; Conservative
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/product-"Df22"

/db_xref-"P1D: 91518051"

/db_xref-"P1D: 91518051"

/db_xref-"P1D: 91518051"

ASPAGGYGVAIPPOPLIACESTITEMCRGIGINUTSFPNEMNHETODEAGLEVHQFW

ASPAGGYGVAIPPOPLIACESTITEMCRGIGINUTSFPNEMNHETODEAGLEVHQFW

PLVEIKCSPDLKFFLCSMTTPICLEDYHKPLPVCRSVCERARSGCAPIMQOYSFEWPE
TDIWMAVWASLCFISTFTVLTFLIDSSRFSYPERPIIFLSMCYNIYSIAYIVRLTVG
RERISCDFEEBAAEPVLIQEGLKNTGCAIIFLLMYFFGWASSIWWVILTLTWFLAAGLK
WGHEAIEMHSSYFHIAAWAIPAVKTIVILIMRLVDADELTGLCYVGNQNLDALTGFVV
                                                                                         APLFTYLVIGTLFIAAGLVALFKIRSNLQKDGTKTDKLERLMVKIGVFSVLYTVPATC
VIACYEYEISHWALFRYSADDSNMAVEMLKIFMSLLVGITSGMWIWSAKTLHTWQKCS
NRLVNSGKVKREKRGNWWYRGKGNETVV" 3 others
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Bhanot.P., Wang,Y. and Nathans,J.
Direct Submission
Submitted (30-JUL-1996) Molecular Biology and Genetics, Johns
Hopkins University School of Medicine, 725 N. Wolfe St., 805 PCTB,
Baltimore, MD 21205, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        634
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Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2085)
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Drosophila melanogaster Dfz2 (Dfz2) gene, complete cds
U65589
                                                                                                                                                                                                                                                                               Length 2831;
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Pred. No. 9.21e-12;
40; Mismatches 127; Indels
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/chromosome="3"
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Nature 382 (6588), 225-230 (1996)
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Drosophila melanogaster
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Similarity 38.8%;
106; Conservative
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1..2085
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TLTTFIIDTERFKYPERPIVFLSACYFWVAVGYLSRNFLQNEEIACDGLLLRESSTGP
PRSCILVELTTFFGMASSIWWYLLFFWFLAAGLKWGNREAITHRGOYFHLAAWLIPTV
QSVAVLLSAVDGDPILGICYGNLNEDHYKTFVLAFLYFLYLJGTTFLAAGFSVSLFF
IRSVIKQQGGVGAGVKADKLEKLMIRIGIFSVLYTVPATIVIGCYLYEAAYFEDWIKA
                 GAGGSSGSTSTKPCRGRNSKNCQNPQGEKASGKECSCSCRSPLIFLGKEQLLQQQSQM
PMMHHPHHWYMNLTVQRIAGVPNCGIPCKGPFFSNDEKDFAGLWIALWSGLCFCSTLM
                                                                                                                                            LACPCAQVKGPGKKPLYSVLMLKYFWALAVGITSGVWIWSGKTLESWRRFWRRLLGAP
DRTGANQALIKQRPPIPHPYAGSGMGMPVGSAAGSLLATPYTQAGGASVASTSHHHLH
RMACEHLPLHGDPDNLCMEQPSYTEAGSGGSSGSSGSGSGSGSGKRKQGGSGSGSG
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Mus musculus putative transmembrane receptor (frizzled 7) mRNA,
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Direct Submission
Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and
Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street,
Baltimore, MD 21205
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42; Mismatches 150; Indels
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/chromosome="2"
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Best Local Similarity 38.5%;
Matches 120; Conservative
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/product-"transmembrane receptor"
/db_xref="PID:g1151258"
/db_xref="PID:g1151258"
/db_xref="PID:g1151258"
/db_xref="MGPFAASHSPLGLCALVLALLGALPTDTRAQPYHGEKGISVP-
DHGFCQPISTPLCTPTAYNOTILPHILGHTWGEDAGLEVHOFYPLVKVQCSPELRFFL
CSMYAPVCTVLDQAIPPCRSLCERARQGCEALMNKFGFQWPERLRCENFPVHGAGEIC
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GYRFLGERDCGAPCEPGRANGLMYFKEEBRRFARLWVGVWSVLSCASTLFTVLTYLUD
MRRFSYPERPIIFLSGCYFWVAVAHVAGFLLEDRAVCVERFSDDGYRTVAQGTKKEGC
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TILAMGQVDEDLISGYCYVGISSVDALRGFVLAPLFYYLFIGTSFLIAGFYSLFRIRT
IMHDGTKTEKLEKLIMVIGVSVLYTYPATIVLACYFYEQAFREHWERTWLLQTKK
YAPOPPRHFSPMSPDPTVFMIKILMYNIVGTTTFRIWSGKTLQSWRFFYHELGHSS
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Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditis elegans
Elkaryotea; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia, Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
I (bases 1 to 1913)
Sawa, H., Lobel, L. and Horvitz, H.R.
The Caenorhabditis elegans gene lin-17, which is required for rectain asymmetric cell divisions, encodes a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| :| | :| | :| | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 
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Submitted (11-JUL-1996) Biology, Massachusetts Institute of
Technology, 77 Massachusetts Avenue, Cambridge, MA 02139, USA
Location/Qualifiers
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Pred. No. 5.54e-10;
44; Mismatches 133; Indels
/gene="frizzled 7"
/note="putative transmembrane receptor"
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Sawa, H. and Horvitz, H.R.
                                                                              /codon_start=1
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Best Local Similarity 39.6%;
Matches 118; Conservative
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/note="Drosophila polarity gene (frizzled) homologue"
/codon_start=1
/db_xref="PlD:g31017"
/db-xref="PlD:g31017"
/db-xref="PlD:g3101
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Zhao, Z., Lee, C.C., Baldini, A. and Caskey, C.T.
A human homologue of the Drosophila polarity gene frizzled has been identified and mapped to 17921.1
identified and mapped to 17921.1
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    Two homologs of the Drosophila polarity gene frizzled (fz) are
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Pred. No. 1.13e-08;
47; Mismatches 124; Indels
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Human frizzled gene product mRNA, complete cds
L37882
                                          xpressed in mammallan tissues
Chem. 267, 25202-25207 (1992)
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1255 c 1220 g 1067 t
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766..2691
                                                                                                                                                                                                                                                                                     /strain="Sprague-Dawley"
/cell_line="UMR106-01"
/cell_type="osteoblast"
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larity 40.6%;
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/db_xref="PID:g1589780"
/translation="MANSLGITLLFIPLAGSIFDQAVGKCIPIDIELCKDLPYNYT
/translation="MANSLGITLLFIPLAGSIFDQAVGKCIPIDIELCKDLPYNYT
PROTILHNOGHTLGTHTEHFRPLMKTKCHPHIHFICSVFAPMCPIGMPQAVTSCKS
VCEOVKADCFSILEEFGIGWEPPLAMKTKCHPHIHFICSVFAPMCPIGMPQAVTSCKS
SSSSKPTGCPSDLVDVDPHDPRSHCAFACQSNVMFSTDNKRMVRSWSIWFAAANAGV
ALFSFLTFAIDRKRFRFPERCVFYLSLCIFISSLPYLTPLFIDAPIRSCHALGNGRSY
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VAWGLSSLATITYLLFNYDASELTALCSYGRUNSTALLWFYVVPRTTCIVIGTCFIV
GGFASWCRERISFRTRGTDTSKLEKLMVKMGFFCALFILDNVIELVCQCYKFMLLTGW
TRWTIDCKQQGGACHRETPPQAEIYWTAVISSLATGFSCLMWVLSARTVHAWKNFIFC
GMCSSAPVKNPIEPSTRPLLEPPTAPPQPPVYMQMATNPQNSWRPSKVV"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 4540)
Chan, S.D.H., Karpf, D.B., Fowlkes, M.E., Hooks, M., Bradley, M.S.,
Vuong, V., Bambino, T., Liu, M.Y.C., Arnaud, C.D., Strewler, G.J. and
Nissenson, R.A.
                                                                                                                                                                                                    /function-"regulates certain asymmetric cell divisions"
/note-"similar to Drosophila Frizzled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RATFRZZH 4540 bp mRNA ROD 16-JUL-1993
Rattus norvegicus Drosophila polarity gene (frizzled) homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 GCNAAYYTNCARYTNTGYCAYGGNATNGARTAYCARAAYATGMGNYTNCCNAAYYTNYTN 132
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frizzled gene; homologue; polarity gene.
Rattus norvegicus (strain Sprague-Dawley) osteosarcoma cDNA
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Pred. No. 1.13e-08;
55; Mismatches 192; Indels
                                                                                'note="SL1 trans-splice leader"
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chromosome="I"
                                                                                                                                                             'gene="lin-17"
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Local Similarity 35.8%;
Nes 138; Conservative
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Matches

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RDAACEPARRDGSMFFSQETRFAMILIYUNDQRRYP
ERPIIFLSGCTHWSVAXIAGFVLQBRYVCHRFSBGGYRTWOGTKREGCTILFWML
YFFSWASSIWWVILSLTWFLAAGMKWGHEAIEANSQYFHLAAWAVPAVKTITILAMGO
IDGDLLSGCYCYGGLSDFLGFYLFFTYFTTILAMGO
IDGDLLSGCYCYGGLSDFLGFYLFTTITATTILAMGO
ITGRLAMRIGYSSYLYTYPATIVLACYFEQDAFREHWERSWYSOHCKSLAIPCPA
HYTPPRASPDFTVYMIKYLMTLIVGITSGFWINSGKTLHSWRRFYTRLINKHGT
                                                                                                                                                                                                                                  PLCTDIAYNQTIMPNLLGHTNQEDAGLEVHQFYPLVKVQCSPELRFFLCSMYAPVCTV
LEQAIPPCRSICERARQGCEALMNKFGFQWPERLRCEHFPRHGAEQICVGQNHSEDGA
                                                                                                                                                                                                                 /translation="MRPRSALPRLLLPLLLPAAGPAQFHGEKGISIPDHGFCQPISI
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Chan, S.D.H., Karpf, D.B., Fowlkes, M.E., Hooks, M., Bradley, M.S.,
Vuong, V., Bambino, T., Liu, M.Y.C., Arnaud, C.D., Strewler, G.J. and
Nissenson, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RATFRZH 1912 bp mRNA ROD 16-JUL-1993
Rattus norvegicus Drosophila polarity gene (frizzled) homologue
mRNA, complete cds.
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J. Blod. Chem. 267, 25202-25207 (1992)
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frizzled gene; homologue; polarity gene.
Rattus norvegicus (strain Sprague-Dawley) osteosarcoma cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 80;
Pred. No. 8.23e-08;
                                                                                                                                              /note="polarity gene; putative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                               356 t
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/clone_lib="fz-2"
                                                                                                                /gene="frizzled"
/function="development"
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                              /tissue_type="ovary"
/chromosome="17"
/map="17q21.1"
133..1830
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Best Local Similarity 39.7%;
Matches 119; Conservative
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MEDLINE
FEATURES
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organism="Rattus norvegicus"

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LEMMLYFFSMASSIWWVILSLTWFLAAGMKWGHAAIEANSQYFHLAAWAVPAVKTITI
LAMGQIDGDLLSGVCEVGLNRLDPLASFYLLAFYYLEIGTSFLLAGFYSLFRTIM
KHOGTKTEPLERLWYLGGYSVLXTYPATYYACYFYEQAFREHWERSWYSGHCKSLA
IPCPAHYTPRTSPDFTYMKYLMTXLMTLIVGITSGFWTNGSGKTLHSWKRYTRLYRSRHG
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                                                                                       /note="Drosophila polarity gene (frizzled) homologue'
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
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Secennentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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CD63 antigen like; Drosophila tissue polarity protein like;
histone H2A; histone H4; Mouse bright protein like;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 1912;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Score 52; DB 90; Le
Pred. No. 5.83e-07;
41; Mismatches 138;
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01-MAR-1997 (Rel. 51, Last updated, Version
                                                   /tissue_type="osteosarcoma"
79..1791
                                                                                                                                                                                                                                                                                                                                                  385 t
/strain="Sprague-Dawley"
               /cell_line="UMR106-01"
/cell_type="osteoblast"
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                                                                                                                                                                                                                                                                                                                                                  266
                                                                                                            /codon_start=1
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larity 39.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transporter protein
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Matches 118; Conser
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MEDLINE; 94150718
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CET23D8
Z81128;
e1008304
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Wild A.;
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ORIGIN
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PEIIGEASMRSFVRNLVNVASEIGMPFLEEHRFCRYAEPDQTVKLLEHLNEQYNLQLV
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/note="Similarity to histone H4"
/db_xref="PID:e275927"
/translation="WSGRGKGGKGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MYELSDDVKRKEWLDDWLNFMHRIGKPVTRIPIMAKQVLDLYEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLVVQHGGLVEIINKKLWREITKGLNLPSSITSAAFTLRTQYQKYLYDYECEKEKLSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(31876..31973,32210..32284,32331..32573,
32640..33032,33192..33264))
/product="T23D8 8"
/note="protein predicted using Genefinder"
/note="Similarity to Mouse bright gene (TR:062431)"
/db_xref="PID:e304447"
Bonfield J., Burton J., Connell M., Copsey T., Cooper J.,
Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A.,
Fulcon L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B.,
A C'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A.,
Studers D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E.,
Studen R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M.,
A Vaughan K., Waterston R., Watson A., Weinstock L.,
Milkinson Sproat J., Wohldman P.;
T.2. Mb of contiguous nucleotide sequence from chromosome III of
C. elegans.;
C. elegans.
C. elegans.
C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both
a dye primer and dye terminator reaction, from distinct
subclones. Exceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="protein predicted using Genefinder"
/note="Similarity to Rat CD63 antigen (SW:P28648)"
/db_xref="PID:e276248"
                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence is NOT necessarily the entire insert of clone T23D8. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true 16ft end of clone T23D8 is at 1 in this sequence. The true 16ft end of clone T23D8 is at 1 in this sequence. The true 16ft end of clone T24D8 is at 1249 in this sequence. The true right end of clone T24D1 is at 12749 in this sequence. Coding sequences below are predicted from computer analysis, and other available information.

The start of this sequence (1..104) overlaps with the end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Caenorhabditis elegans"
/clone="T23D8"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,10019..10101,10150..10212))
/product="T23D8.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(25597..25908)
/product="T23D8.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Key
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VESAWDKTHQLFECCGVTNSSDWLTFTT1PDSCC1EE1EGCARENAPLFEPGC1HSVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNLDYNQTVFPNLLGHTTQSEAGPAIAQFNPLIKVKCSEDIRLFLCTVYAPVCTVLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQPCRELCLSAKNGCESLMKKFGFQWPDQLDCNKFPVTDLCVGKNSSESSNSKKSSND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TFGVSTIANEVVLSPKKCPHHMHTTSGSHFSLPLLSGRLPECSLTCEADNQVPMMFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /RRILRIWTAAWSVACFVCSLFTLVTFLVDLSRFAYPVRPILYLAFCYLAISTVYMIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGEDGFACGTYGSTPTTLVTQGGENVGCSALAVVHYFFFMSSCAWWLVLCLAWFLAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KWGAESIAALSPYFHAMCWGVPAVLSVTVLVTNSVDGDVFTGICSVGNLNPSALVYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPIVVSLALGAVLLVCGIWSMIRIRSYIKLQHADVERNISKLEKLMLRIGAFAIMYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAMNAAIMWYQAVNMPAWLEGWLHHRCVRLQDRELFGFTYPVDDCPMDPKVAAPEIIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSGRGKGGKAKTGGKAKSRSSRAGLQFPVGRLHRILRKGNYAQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MEDQWLLSAlYDDDLVEKLKVRSSTSSRSTSINVPSLENEFLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGSRVSDDLYLHPIEENREPFKLIGKPLPSTTGRFLSLLANHFQITCNGSIIHQYYIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPDIPSKKLNRTILRTLQEQNPGLIECPLVFDGIHTVYSTELINVKEVNNSVINVAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTKESPNLFKLYLTHVDSFLLDTKIITGNQDQNQKLRMMHAIDTVFRQTSTGNFHAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFFSIAQNSAIEPSHGLGWGTVNLGVGREVCYGFYQNVVETFDTLTMNLDVATTTFYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /ALVEFLAEILEVPLATVTDGRSLSDVQKKKFNREVAGLKVETRHCSCPRRFRVARCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPTENISFHLSETAGNQDSKPLSLVEYYKRRYNIDLTYKHLPCIEVGRTRECILPLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVVSGQRCIKKLNEQQIANLIRATSRNATERQNAVMSLQNRLKMDNDVNAVKFGLKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLLKIEGRVLPVPRLLYRSPNLKRQECVTVPNNGTWDMRGKNFYSGIQIREWAIVCFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAPVYLAAVLEYLAAEVLELAGNAARDNKKTRIAPRHLQLAVRNDEELNKLLAGVT
                                                                                                                                                                                                                                                                                        /note="protein predicted using Genefinder"
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(TR:024760)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLKYVSQLVVGITCAIWVVSSKTLSSYHKAYLALSSRSPTVPAHVDQVNMR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQGGVLPNIQAVLLPKKTGGDKE"
                                                                                                                                                                                                                            ,5688..5906,6332..6479)
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Washington University,
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                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
COMMENT
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                                                                                                                                                                                                                        TITLE
CIVPGKSVVYGELKRKGELLGLTTQCVRSQNVSKASPHTLSNLCMKINSKLGGINVIL
                                                             IQPRHQRIIVDMCEMTREAIINFRKSTGFKPHKIIIYRAGIADVTVDEIMQTELRAVR
                                                                                             ACAMIEYGFQPGITFIGLDVTHHTRLFAANEKDRVGNSQNVPAGTLVETGITVNNLFE
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                                                                                                                                                                                                                                                                                                                                      IDDDYDYLQHMRAVNEPMKLENVHEEVEKTTIKTSGSSAFPPAPPLFGLVGALKKPEF
                                                                                                                                                                                                                                                                                                                                                                        DEDVANALEEVTDDRNTGELEDNFITLAGGLLDERTTVYRSTRRGEDSEEEEDDDEDD
                                                                                                                                                                                                                                                                                                                                                                                                      MYDDYNDDELFGEEAVGEIRVERADORVIDNAFEELMDREYNTDQIGELDGDDYDVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (21-OCT-1996) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RQ, England and Department of Genetics,
                               SPPQSLNSEPVLFIGCHLTRSSLASSSDSTSSIAHCDSSIACLVGSMDGHPTQFSPIF
                                                                                                                                                                                                                                                                                                                                                                                                                                     LEPNAGRLHKLINDKGPSNAEYDEELAKHYVRERMRLIEBGVIKDKEEYEIVEVDEGT
                                                                                                                                                           2910 ttccaatgtgcaaaaatctggattacaatcaaacagtatttccaaatcttctcggacata 2969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3029 igcicagaagataticgictititititgiacigiciaigcaccigicigiacag-i-ac 3086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 TGYCAYCCNGAYACNAARAARTTYYTNTGYWSNYTNTTYGCNCCNGTNTGYYTNGAYGAY 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-1996
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Caenorhabditis elegans
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea: Rhabditia; Rhabditida; Rhabditidae;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 CCNGINAIGWSNGCNIIYGGNIIYCCNIGGCCNGAYAIGYINGARIGYGAYMGNIIYCC
                                                                                                                                                                                                                       /note="protein predicted using Genefinder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52; DB 8; Length 34576; Pred. No. 5.83e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 40.1%;
Matches 120; Conservative
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ACCESSION
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TITLE
JOURNAL
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Nature 368 (6466), 32-38 (1994)

Nature 368 (6466), 32-38 (1994)

B 94150718

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of clone T23D8. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone T23D8 is at 1 in this sequence. The true right end of clone T23D8 is at 34576 in this sequence. The true right end of clone T24D1 is at 12749 in this sequence. Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green, ms in preparation), and other the start of this sequence (1..104) overlaps with the end of sequence (EET241).
                                                                       C (bases I to 34576)

S Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,

Bonfield, J., Butron, J., Connell, M., Copsey, T., Cooper, J.,

Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,

Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,

Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,

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Staden, R., Sulston, J., Thierry Mieg, J., Thomas, K., Vaudin, M.,

Vaughan, K., Waterston, R., Waterston, R., Weinstock, L.,

Wilkinson-Sproat, J. and Wohldman, P.,

Wilkinson-Sproat, J. and Wohldman, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLAANLKWGAESIAALSPYFHAMCWGVPAVLSVTVLVTNSVDGDVFTGICSVGNLNPS
ALVYFFFTPIVVSLALGAVLLVCGIWSMIRIRSYIKLQHADVERNISKLEKLMLRIGA
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RGVESAWDKTHQLFECCGVTNSSDWLTFTTIPDSCCIEEIEGCARENAPLFEFGCIHS
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St. Louis, MO 63110, USA. E-mail:
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1..34576
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                                            jes@sanger.ac.uk or rw@nematode.wustl.edu
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join (26949. 270468.27120. 27187, 27232. 27606, 27661. 28621,
28689. 28819, 29049. 29748, 30273. 30464, 30510. 30659)
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281128
91628237
CD63 antigen like; Drosophila tissue polarity protein like; histone
                                                                                                                                                                                                                                                                                         /translation="MSNFFLGIKVNNRLLTINWSPIRIIVFLDSFFDSDNSLLLFFLV
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Ad_xxef="PID:g1628239"
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              SGAVPLVMNSQIVNMAEHSTLSQSFLIINILLILILIFVVGMLDAHHVHFANFVFIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2910 ttccaatgtgcaaaaatctggattacaatcaaacagtatttccaaatcttctcggacata 2969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3087 t-cgaaaaaccaattcaaccatgtcgagaattgtgtttatctgcaaaaaatggatgcgag 3145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 INCARYINIGYCAYGGNAINGARTAYCARAAYAIGMGNYINCCNAAYYINYINGGNCAYG 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3146 tcattaatgaaaaagtttggatttcaatggccagatcaattggattgtuacaaattccc 3204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 CCNGTNATGWSNGCNTTYGGNTTYCCNTGGCCNGAYATGYTNGARTGYGAYMGNTTYCC 377
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Pred. No. 5.83e-07;
44; Mismatches 130; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26277...26660
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                                                                                                          /note "protein predicted using Genefinder"
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                                                                                                                                                                              /product="T23D8.j"
/db_xref="PID:e275932"
/db_xref="PID:g1628247"
                                                                                                                                                                                                                                                                                                                                                                                            complement(25597..25908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"T23D8.b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: remainder of annotations omitted.
                                          ARIVTKFNVLLGLFNE"
15774..16091
                                                                                                                                                 /codon_start=1
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Best Local Similarity 40.1%;
Matches 120; Conservative
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/code="procein predicted using Genefinder"
/code="procein predicted using Genefinder"
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FFDEDVANALEEVTDDRNTGELEDNFITLAGGLLDERTTVYRSTRRGEDSEEEEDDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDEMYDDYNDDELFGEEAVGETRVERADGRYIDNAFEELMDREYNTDQIGELDGDDYD
VGGALENARGHLHKLINDKGPSNAEYDEELAKHYVBEWRLIEBGYIKDKEEYETYEV
DEGTNKKMKWORGESFAYTNIYNHPTLIKEPRGLSRRALFREDAAVEEMDIABEDED
DDEDWEDDDDDKESVFSTYGTRRKNEFPEQRSLRAKKARVERKRUKTWHFAE
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Rat CD63 antigen (SW:P28648)"
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KRDIQPCRELCLSANKGEGPAIAQFNPLIKVKCSEDIRLFCTVTRVTPCTVET
KPIQPCRELCLSANKGESLAKKFGFQWPDQLDCNKFPYDLLVGRNSSESSNSKKS
NDVTFGVSTIANEVVLSPKKCPHMHTTSGSHFSLPLLSGRLPECSLTCEADNQVPMM
FMGTVVGEDGEATTVTFLYTOFTUTFFLVBTSTTATTSTY
MIGVVGEDGEATTGSTPTLLVTQGGENVGCSALAVVHYFFFRASCAMMIVLCLAM
FLAANLKWGAESIAALSPYFHAMCWGVPAVLSVTVLVTNSVDGDVFTGICSVGNLNPS
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The true left end of clone T23D8 is at 1 in this sequence. The true right end of clone T23D8 is at 15749 in this sequence. The true right end of clone T24D1 is at 12749 in this sequence. Coding sequences below are predicted from computer analysis, using the available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALVYFFFTPIVVSLALGAVLLVCGIWSMIRIRSYIKLQHADVERNISKLEKLMLRIGA
FAIMYSLPTAMNAAIMWYQAVNMPAWLEGWLHHRCVRLQDRELFGFTYPVDCPMDPR
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5220..5340,5688..5906,6332..6479)
/note="protein predicted using Genefinder; Similarity to
Drosophila Tissue polarity protein (TR:024760)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of
         histone H4; Mouse bright protein like; transporter protein
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9211..9343,10019..10101,10150..10212))
/note="protein predicted using Genefinder; Similarity
                        Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditiaa; Rhabditia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Caenorhabditis elegans"
/clone="T23D8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368 (6466), 32-38 (1994)
94150718
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Location/Qualifiers
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                                                                                                       ORGANISM
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
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MEDLINE
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Complement(join(13883..14240,14292..15409,15456..16341, complement(join(13883..14240,14292..15409,15456..16341, 16423..16656,16705..16807,1768..17721,1774..18278, 18330..18656,18888..19113,19170..19705,19751..19828, 19844..19991,20041..20214), note="Similarity to Yeast nuclear transport protein (SW:P32497); conex from this gene; conex from this gene...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIGSTRIAND TRANSPORTED TO THE TOTAL THE TOTAL TRANSPORTED TO THE TOTAL THE THE THE TOTAL TRANSPORTED TO THE TOTAL THE THE TOTAL TRANSPORTED TO THE TOTAL THE TOTAL TRANSPORTED TO THE TOTAL THE TOTAL TO THE TOTAL TRANSPORTED THE THE THE THE TOTAL TO THE TOTAL TRANSPORTED THE TOTAL THE TOTAL TRANSPORTED THE TOTAL THE TOTAL TRANSPORTED THE TOTAL TO THE TOTAL TRANSPORTED THE TOTAL TO THE TOTAL TRANSPORTED THE TOTAL TRANSPORTED THE TOTAL TO THE TOTAL TO THE TOTAL TRANSPORTED THE TOTAL THE TOTAL TRANSPORTED THE TOTAL TO THE TOTAL TRANSPORTED THE TOTAL THE TOTAL TRANSPORTED THE TOTAL TRANSPORTED THE TOTAL TRANSPORTED TOTAL TRANSPORTED THE TOTAL TRANSPORTED TO THE TOTAL TRANSPORTED TOTAL TRANSPORTED TOTAL TRANSPORTED TO THE TOTAL TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                     VEQWYLKNGAWYGGICAVLAAIQLVGYCFACCLSKSILKDFHDFYY"
complement(join(10723..10767,11212..11658,11707..11823,
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/note="protein predicted using Genefinder; cDNA EST cm16f9
comes from this gene; cDNA EST CEESF93R comes from this
gene; cDNA EST CEESF93FC comes from this gene"
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FFDEDVANALEEVTDDRNTGELEDNFITLAGGLLDERTTVYRSTRRGEDSEEEEDDDE
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DEGTNKKMKWDCESFATQYTNIYNHPTLIKEPRGLSRKALKRFDKAVEEMDIAEEDED
DDEDMEDDDDKESVFSTVSTFRPKNETPEQRSLRKKAVKEARKLRRVEKKANKTMFAE
                                                                                                                                                                                                                                                                                          LGDERLATPILLLVIGSLCTLLGFLGCCGAIRENYCLTVSFAVLLALLITGWVRYHES
RGVESAWDKTHQLFECCGVTNSSDWLTFTTIPDSCCIEEIEGCARENAPLFEPGCIHS
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FRELICNLISLMWQKDPHMKHCANQVFQIFNCIIMGVKNEKLRTEFAQHLKFEKLVGT
LSEYFNPQVHPGMINPAIFIIFRFIISKDTRLKDYFIWNNNPHDQPPPPTGLIIKLNA
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NAKISDHMEYETFWTTLQTVNSLLDLLIGTDRVKLSVTYAÆEDENLKDDTQEYRIQGS
ILIAVQRLDGELAKILQNADCHSNDYIEKLKAEKDMCSLIEKAEKYVELRNDSGIFDK
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EIQNTQRAKELLAQAVGTRQHEKTAEQEKIDRSRQVPYHMHINVELMECVYLICSMLL
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SQGGQQRRHPQKPRAF"
                                                                    /db_xref="PID:e276248"
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/product="T23D8.2"
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                                                                                                                                                                                                Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
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5 107:EST107 108:EST108 105
117:EST112 113:EST113 113
1122:EST112 118:EST118 113
1122:EST122 123:EST123 125
1137:EST137 128:EST123 125
1137:EST137 138:EST133 125
1137:EST137 138:EST133 125
1142:EST142 143:EST143 147
1142:EST147 148:EST148 147
1142:EST147 148:EST148 147
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1142:EST147 148:EST148 147
1142:EST167 158:EST168 116
1142:EST167 168:EST168 117
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156:EST156
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Perfect Score:
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B Human aorta CDNA 5'-e 0.00e+00
YLZG03.3 Homo sapie 0.00e+00
YLZG03.3 Homo sapie 0.00e+00
YS74c07.31 Homo sapie 0.00e+00
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                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 179:EST179
184:EST184
189:EST189
194:EST194
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human clone=278321 primer-mob.REGA+ET library-Soares multiple
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mAL1f02.rz Soares mou 1.5
HUMGS0005382, Human G 1.11
ym31e03.r1 Homo sapie 1.12
JU9816F Homo sapiens 1.12
15684.seq.F Fetal hea 3.5
c10685.seq.F Fetal hea 2.2
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178:EST178 1 183:EST183 1 188:EST188 1 193:EST183 1 198:EST193 1
                                          scale 4.307
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Homo sapiens cDNA clone 278321 5'
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175:EST175 176:EST176 177:EST177 180:EST180 181:EST181 182:EST182 182:EST182 196:EST190 191:EST197 195:EST195 196:EST195 1
                                          Variance 2.824;
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48 HUM240B02B H1

48 HUM289F09B H1

1 110 HUM343G04B 1

8 48 HUM233G01B H1
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HUM286A04B
HUM224H07B H
HUM351F11B H
HUM221G02B H
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HUM303B01B
HUM304B12B H
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W72225
W32415
W32412
H87071
H16121
HUM296807B
AA024771
H44092
H15818
H1618
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H87723
HUM325D05B
W08345
C02046
H29095
N56478
AA095691
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HUM307G04B
HUM238C04B
HUM238C05B
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HUM229D08B
                                                                                   SUMMARIES
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterayil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 480)
11 (bases 1 to 480)
12 (bases 1, Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Hollman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est(@watson.wustl.edu
High quality sequence stops: 393
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1396 AIGAATATTTTATGAAGTTTAAAAATAGCTCACTTTAAAAGCTAGTTTTGAATAGGTGCA 1455
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normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
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                        1756 ATTTCTAFAGCAFGATTCTTCAAGTAAAAGGCAAAAGATAAAATTTATATAATTGACTT 1815
                                                                                                                      1816 GAGTACTTTAAGCCTTG-TTTAAAACATTTCTTACTTAACTTTTGCAAATTAAACCCAFT 1874
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2d70e11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
346028 3'.
W72225
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Eukaryotae; mitochondrial eukaryotee; Metazoa; Chordata;
Eukaryotae; mitochondrial eukaryotee; Metazoa; Chordata;
1 (bases 1 to 460)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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361 atttctatagcatgatttcttcaagtaaaaggcaaaagatataaatttataattgactt
                                                                                              421 gagtactttaagccttggtttaaaacatttcttacttaacttttgcaaattaaacccatt
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Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterorygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 446)
Hillar, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlifing, T., Soares, M., Tan, F., Taryaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 225
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (Info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                          1627 CIGATGAAGATGTTGAGATAACAGCCAGCTTTATCTCAACAGGGTTTGTGACCCACAAGT 1568
1806 ATAAAATTTATATCTTTGCCTTTTACTTGAAGAAATCATGCTATAGAAATGTTAATGT 1747
                                                                                                                                                                                                                          1866 TAATTTGCAAAAGTTAAGTAAGAAATGTTTTAAACAAGGCTTAAAGTACTCAAGTCAATT 1807
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                                                                   121 taatttgcaaaagttaagtaagaaatgttttaaacaaggcttaaagtactcaagtcaatt
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This clone is available royalty-free through LLNL ; contact the
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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WashJ-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                          Score 416; DB 101;
Pred. No. 0.00e+00;
0; Mismatches 1;
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/organism="Homo sapiens"
/clone="278321"
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IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1550 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 424.
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9
                                                                                                                                                                                                                                                                                  Score 413; DB 174; Length 462;
Pred. No. 0.00e+00;
0; Mismatches 3; Indels 6
                                                                                                                                                                                                                                                        others
                                                                                                                                                                                                                                /clone_lib="Soares fetal heart NbHH19W"
/sex="unknown"
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98.0%;
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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                       Eukaryotes, Metazoa, Eumetazoa, Bilateria, Coelomata,
Eukaryotes, Metazoa, Eumetazoa, Bilateria, Coelomata,
Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes,
Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria,
Eutheria, Archonta, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 445)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                  σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
High quality sequence stops: 314
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from
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Rsite2=Eco RI two placentae: one from 8 weeks and another fro
weeks post conception. 1st strand cDNA was primed with a Not
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                                                                                     oligo(dr) primer
[5/-rgrraccaarcrgaaGrggGaGcGGCGGGATTTTTTTTTTTTTTTTTTT-3/],
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washu-Merck EST Project
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 0.00e+00;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Seg primer: -40M13 Fwd. from Amersham
High quality sequence stop: 289.
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heart NbHH19W Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 433), Hillier, Elliston, K., Hawkins, M., Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
WashU-Werck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels 1;
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/lab_host="DH10B (ampicillin resistant)"
complement(<1..>433)
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/clone_lib="Soares fetal heart NbHH19W"
/sex="unknown"
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Pred. No. 0.00e+00;
0; Mismatches 2;
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                            421 ttgtgacccacagttttgg 440
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ilarity 99.2%;
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Matches 369; Conserv
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H87071 21-NOV-1995
ys74d07.rl Homo sapiens cDNA clone 220525 5' similar to SP:A45054
A45054 Fz-1=PUTATIVE INTERCELLULAR SIGNAL TRANSDUCER OR TRANSMITTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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Washu-Marck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 355
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                 1880 AGCTACAATGGGTTTAATTTGCAAAAGTTAAGTAAGAAATGTTTAAACAAGGCTTAAAG 1821
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agctacaatgggtttaatttgcaaaagttaagtaagaaatgtttaaacaaggcttaaag 180
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                                                                                                                                                                              Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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                                                                                      407 ACGCCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCATGAAGG 466
                                                                                                             aggtgctggagcaggccggcgcttggatcccgctggtcatgaagcagtgccacccggaca 121
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                            'n
                      Length 426
                   Score 359; DB 72; Length 42
Pred. No. 0.00e+00;
0; Mismatches 17; Indels
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WashU-Merck EST Project
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Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 340)
Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E.-I., Hirai,Y., Unpublished(303)
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Tel: 314 286 1800
Fax: 314 286 1810
Fmail: est@watson.wustl.edu
High quality sequence stops: 321
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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HUMZA GOTTA CDNA 5'-end GEN-296B07.
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/clone="159560"
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Submitted (30-May-1995) to DDBJ
Tsutomu Fujiwara
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Best Local Similarity 98.1%;
Matches 368; Conservative
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Best Local Similarity 92.5%;
Matches 368; Conservative
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                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:323325
                                                                                                                                                                                                                                                        1616 CATCTTCATCAGCTCCAGACTGAGACTCAGTGTCTAAGTCTTACAACAATTCATCATTT 1675
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                             polyA+ mRNA (#6572)"
3 others
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                                                                                                                                                             Length 340;
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WashIngton University School of MedicineP
WashIngton University School of MedicineP
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 gttgtaaaartattgctttraccaacactgtaaatatttc 340
                                                                      /organism="Homo sapiens"
/clone_lib="Clontech human aorta
64 c 38 g 122 t
                                                                                                                                                         Score 331; DB 48;
Pred. No. 0.00e+00;
3; Mismatches 1.
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                                             Location/Qualifiers
                                                                                                                                                         ch 16.3%;
il Similarity 98.5%;
335; Conservative
           Phone: 0886-65-2888
Fax : 0886-37-1035
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Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhin; Hominidae; Homo.

I (bases 1 to 414)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Klocaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rikkin,L., Rohlfing,T., Soarss,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                              /clone_lib="Stratagene mouse heart (#937316)"
/sex="pooled"
/dev_stage="13 day embryos"
                                                                                                                                                                                                                                                                                                                                              Score 328; DB 178; Length 396;
Pred. No. 0.00e+00;
0; Mismatches 28; Indels 2
                                                                                                                                                                                                                                       /lab_host="SOLR (kanamycin resistant)"
<1. >396
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/organism="Mus musculus"
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                                                                                                                                                                /clone="536389"
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FEATURES

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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 434)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Source: INAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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numan clone=183540 library=Soares breast 3NbHBst vector=pT7T3D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washu-Merck EST Project
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality_sequence stops: 123
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/clone="183540"
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ilarity 93.5%;
Conservative
                                                                                                                                                                                                                     and M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
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                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 288.
Location/Qualifiers
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/clone_11b="Soares fetal heart NDHH19W"
/sex="unknown"
/dev_stage="19 weeks"
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Homo sapiens cDNA clone 183540 5'
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Pred. No. 0.00e+00;
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WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: estewatson.wustl.edu
High quality sequence stops: 340
Source: IMAGE Consortium, LLNL.
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Y12805.s1 Homo sapiens CDNA clone 159560 3'
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Pred. No. 0.00e+00;
0; Mismatches 3;
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Best Local Similarity 97.1%;
Matches 370; Conservative
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                            1909 TTAAAAGTTGTAA 1921
422 ttaaaagtggtaa 434
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Deuterostomia; Chordata; Vertebrata; Gnathostometa; Osteichthyes;
Sarcoptersygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 326)
Hillaer, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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High quality sequence stops: 312
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Pred. No. 0.000+00;
....matches 0; Indels 1; Gaps
                    1762 TAGAAATGGTTAATGTGCTTCTAATAAATGG-AAGTATTGTAG-CTGG-AATGTGATACA
                                                                                                                        1705 IGTAACAGTITAAG-TICCCATIGAAGG-TATAAAATGAIGAATIGITGIAHHHH HHH
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                              326 bp mRNA EST Homo sapiens cDNA clone 258852 3'.
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WashU-Merck EST Project
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E.-I., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
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                                                  1939 TIGGITAAAGCAATATITITACAACTITITAAAGGTAAAACTACTATGTATATACAGGTAA 1880
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57 c 32 g 118 t 7 others
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larity 97.8%; Pred. No. 0.00e+00;
Conservative 6; Mismatches 0; Indels
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Submitted (30-May-1995) to DDBJ by:
Tsutown Fuliwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho
Tokushima, Tokushima
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Fax : 0886-37-1035
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COPYL	(c) 1993, 1994, 1993 University 1stribution rights by Intelligenet		വവ	145 145		mw14c07.rl Soares mou mw14c07.rl Soares mou	
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ır output	. pg	20		262	AA176165 HS1145682	zp23h12.s1 Stratagene	2.36e-
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	84:enEST10 85:enEST11 86:enEST12 87:enEST13 88:enEST14 89:enEST15 90:enEST16 91:enEST17 92:enEST18 93:enEST19	KEYWORDS	EST.				
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	103:enEST29 104:enEST30 105:enEST31 106:enSTS 107:ueEST1 108:ueEST2	REFERENCE	Vertebrai	ta; Eutheria	a; Primates;	yotes, metasoa, choitaa Catarrhini, Hominidae	HOMO.
Statistics:	Mean 12.177; Variance 2.973; scale 4.096	AUTHORS	Hillier, I Holman, M	L., Clark, N ., Hultman,	., Dubuque, T M., Kucaba, T	., Elliston, K., Hawkins, M., ., Le, M., Lennon, G., Marra, M.,	s, M., arra, M.,
Pred. No. score gree and is der	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.	TITLE JOURNAL	Farsons, waterstor WashU-Men	J., Ritkin, J.R., Willic rck EST Proj hed (1995)	L., Rohling amson,A., Wo ject	Parsons,J., Kirkin,L., Rohling,T., Tan,F., Trevaskis,E. Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashU-Merck EST Project Unoublished (1995)	ж ж 
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Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine

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                                                                             Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1171 Std Error: 0.00
Seq primer: -40M13 fwd, from Amersham
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Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 0.00e+00;
0; Mismatches 2; Indels
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/lab_nost="DH10B (ampicillin resistant)"
complement(<1..>505)
1 of c 100 g 162 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="366083"
/clone_lib="Soares fetal heart NbHH19W"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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1 Similarity 99.0%;
498; Conservative
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Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 682 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 389.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Constant and setting a setting and the setting as the fetal lung library, soares fetal lung same fetus as the fetal lung library, soares fetal lung same fetus as the setting and the setting 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
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W92531 505 bp mRNA EST 25-NOV-1996
ze03g10.rl Soares fetal heart NbHH19W Homo sapiens CDNA clone
357954 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 505)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 atttttatgaagtttaaaaatagctcactttaaaggctagttttgaataggtgcaactgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1462 ACTIGGGTCTGGTTGGTTGTTTTTTTTTTTGAGTCAGCTGATTTTCACTTCCCACTG
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/clone_lib="Soares fetal heart NDHH19W"
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Pred. No. 0.00e+00;
0; Mismatches 2.
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Local Similarity 98.8%;
Les 498; Conservative
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Marra, M. Hillar, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                            1522 AGGTTGTCATAACATGCAAATTGCTTCAATTTTCTCTGTGGCCCAAACTTGTGGGTCACA 1581
                                                                                                                                                 1402 ATTTTTATGAAGTTTAAAAATAGCTCACTTTAAAGCTAGTTTTGAATAGGTGCAACTGTG 1461
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AA105749 g1654838
                                                                                                                 1 atttttatgaagtttaaaaatagctcactttaaagctagttttgaataggtgcaactgtg
                                                                                                                                                                                                                                                 aggttgtcataacatgcaaattgcttcaattttctctgtgggcccaaacttgtgggtcaca
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                   4;
                                                     Length 505;
                                                                                  2; Indels
                  C; 81 G; 180 T; 0 other;
                                                Score 472; DB 90;
Pred. No. 0.00e+00;
0; Mismatches 2;
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Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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                  95
                                                Query Match 23.3%;
Best Local Similarity 98.8%;
Matches 498; Conservative
   mRNA <1.,>505
Sequence 505 BP; 149 A;
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/clone="357954"
/clone_lib-"Soares fetal heart NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
 1642 TCAGIGICTAAGICTTACAACAATTCATCATTITATAACCTTCAATGGGAACTTAAACIGT 1701
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Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
"The WashU-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: St. Louis, MO 63108 Tel: 314 286 1800 Ext. 314 286 1810 Email: LINL: contact the IMAGE Consortium (info@lmage.llnl.gov) for further information. Insert Length: 682 Std Error: 0.00 Seq primer: Rey. Location/Qualifiers
                                                               tcagigicitaagicitacaacaaticatititatacciticaatgggaacttaaacigi
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28-FFB-1997 (Rel. 51, Last updated, Version 2)
2e03g10.rl Soares fetal heart NDHH19W Homo sapiens cDNA clone 357954 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 396)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                 Washurith Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:323325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Stratagene mouse heart (#937316)'
/sex="pooled"
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Pred. No. 0.00e+00;
0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                   1..396
/organism="Mus musculus"
                                                                                                      The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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Best Local Similarity 92.5%;
Matches 368; Conservative
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                                                                                                                        Unpublished (1996)
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| 126 c
                                                                                        Waterston, R.
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BASE COUNT
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                     AUTHORS
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                                                                                                                 /organism="Mus musculus"
/strain="C57/R16"
/strain="C57/R16"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xho!, Cloned undirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTGGGCACGAG 3' ~3' adaptor sequence: 5'
/Clone="518668"
/clone="518668"
/clone="518668"
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 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGT:312516
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       655
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 458;
                                                                                                                                                                                                                                                                                                                                                                                               Score 366; DB 33; Length 45
Pred. No. 0.00e+00;
0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                         /sex="females"
/dev_stage="4 weeks"
/lab_host="SOLR (kanamycin resistant)"
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                                                 Seg primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 457.
Location/Qualifiers
1..458
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18.1%;
Best Local Similarity 91.8%;
Matches 424; Conservative
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Length 396;

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KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

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Contact: Wilson RK
WashD-Merck EST Project
WashIngton University School of Medicine
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA082155 287 bp mRNA EST 01-FEB-1997 ze88ff06.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 366083 5'. AA082155 g1624408
                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 287)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Washu-Merck EST Project
Unpublished (1995)
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/lab_host="DH10B (ampicillin resistant)"
<1...>287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib-"Soares fetal heart NDHH19W"
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Pred. No. 0.00e+00;
0; Mismatches 4;
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t
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/organism="Homo sapiens"
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Local Similarity 97.5%;
les 273; Conservative
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                        AA176165 262 bp mRNA EST 30-DEC-1996 zp23h12.s1 Stratagene neuroepithelium (#937231) Homo sapiens CDNA CA176165 g1757287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
WashU-Merck EST Project
WashU-Merck EST Project
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 161.
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                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 262)
Hillier, L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Wasterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggtaaaacaggatgtaaagtttatatacaagaatataatgtttatctgaaatatttacag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Stratagene neuroepithelium (#937231)"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
complement(<1..>262)
7 c 40 g 91 t 4 others
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Pred. No. 0.00e+00;
0; Mismatches 5; Indels
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Best Local Similarity 98.1%;
Matches 257; Conservative
                                                                                                                                                                                                                                          Homo sapiens
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               through one round of normalization, and was constructed by
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                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:452086 Seq Primer: -28ml3 rev2 ET from Amersham. Rey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                  19-MAR-1997 (Rel. 51, Last updated, Version 1)
va52g08.rl Soares mouse 3NME12 5 Mus musculus cDNA clone 735038 5'
                                                                                                                                                                                                                                                                                                        Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubnque T., Gelsel S., Kucaba T., Lacy M., Le M., Martin J., Ororis M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylle T., Lennon G., Soares B., Wilson R., Waterston R.;
                                                                                                                                                                                                               Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bento Soares and M. Fatima Bonaldo./clone="735038"
                              1207 GAICTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTC 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 17;
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/lab_host="DH10B"
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Pred. No. 0.00e+00;
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            240 gateteagetecegtteee-aageacacteetagetgete
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                                                                                  JT 8
MMAA60087 standard; RNA; EST; 394
AA260087;
91896590
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19-MAR-1997 (Rel. 51, Last upd
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94.18;
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Theses 1 to 523)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisch,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                        1036 GGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGGTGGCAGAAGGGGCAG 1095
                                                                                                                                                                                                               AA122822 523 bp mRNA EST 16-FEB-1997
mr03c11.rl Soares mouse 3NbMS Mus musculus CDNA clone 596372 5'
AA122822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:361804
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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181 ggacagaagcagggcgggcgagctggtgatcacctccgtgaaacggtggcagaagggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Pred. No. 0.00e+00;
0; Mismatches 88; Indels 13;
                                                                                                                                        1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTAGT 1144
                                                                                          241 agagagttcaagcgcatctcccgcagcatccgcaagctgcaatgctagt
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/sex="male"
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Location/Qualifiers
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/lab_host="DH10B"
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Best Local Similarity 80.2%;
Matches 408; Conservative
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M., Hillier L., Allen M., Bowles M., Dietrich
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Best Local Similarity
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 21-NOV-1996
musculus cDNA clone 596372
                                                                                  1077 GCGGTGGCAGAAGGGGCAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCA
                                                                                                                                                                                                                                                                                                                                  1137 GIGCTAGICCCGGCAICCIGAIGGCICCGACAGGCCIGCICCAGAGCACGGCIGACCAII
                                                                                                                                                                                                                                                                                                                                                                                        tccgctccgcgacctcatttccggtttcccaagcacagtccgggaaagctacagcccag
                                                                                                                                                                                                                                                                                                                                                                                                                                              1197 TCTGCTCCGGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCT-GCTCCAGTCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggccctaggaggccttggaaacccatagctgttttcacggaaagcgaaagcccatccag
                                                         gctccgtatctggtcatgggacagaagcagggcggcgagctggtgatcacctccgtgaa
                                                                                                                                                                  acggtggcagaagggccagagagagttcaagcgcatctcccgcagcatctgcagctgca
                                                                                                                                                                                                                                                                              atgctagtttcccagtggggtggcttctctccatccaggccctgagctctgtagaccact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
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mouse 3NbMS Mus
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
Unpublished (1995)
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mr03c11.rl Soares m
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Mus musculus
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3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pp773 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Clone="596372" /clone="596372" /clone="11b="Soares mouse 3NbMS"
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                                                                                                                                                                                                                                                                                                                                                                 Score 242; DB 6; Leuy...
Pred. No. 0.00e+00;
....matches 88; Indels 13;
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
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27-APR-1996 (Rel. 47, Created)
05-MAR-1997 (Rel. 51, Last updated, Version 2)
mb41f02.rl Soares mouse p3NMF19.5 Mus musculus
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/lab_host="DH10B"
<1..>523
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1 Similarity 80.2%;
40%; Conservative
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="vector: pdwV-SPORT; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Gastrulating embryos were collected at 7.5dpc from C57BL6 x DBA matings, excluding embryos that had developed head folds and all extraembryonic tissues. Average insert size: 1.3 kb (range: 0.5 - 3.0 kb). Referenced in Development 121, 2479-2489 (1955)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:341673
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mouse 3NME12 5 Mus musculus cDNA clone 670668
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Washington University School of MedicineP
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0; Mismatches 10;
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                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                    The WashU-HHMI Mouse EST Project Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL6 x DBA"
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/lab_host="DH12s"
<1..>184
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Matches 172; Concerning
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                                      AUTHORS
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Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                              Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wastl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:213395 Seq Primer: mob.REGA+ET High quality sequence stop: 280. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 catcccctcgctagtagcgaccacctcctgccggccacagaggaagctcccaaggtgtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Moris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 209; DB 94; Length 299; 89.8%; Pred. No. 7.57e-286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minoru Ko (Wayne State University)."
/clone="331995"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 A; 95 C; 72 G; 53 T; 0 other;
                                                                                                                                                                                                                                                                                                                                 /organism-"Mus musculus"
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                                                                                            "The WashU-HHMI Mouse EST Project";
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Matches 264; Conserv
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g1808152
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                                                                                                                Unpublished.
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DEFINITION
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                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
Washlo-HHMI Mouse EST Project
Washlordon University School of MedicineP
Washlordon University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@mage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1859 GCAAATTAAACCCATTGTAGCTTACCTGTAATATACATAGTAGTTTACCTTTAAAAGTTG 1918
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1 (bases 1 to 145)
Marraw, Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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AA230899;
91853194
27-FEB-1997 (Rel. 51, Created)
27-FEB-1997 (Rel. 51, Last updated, Version 1)
mw14c07.rl Soares mouse 3NME12 5 Mus musculus cDNA clone 670668
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
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/lab_host="DH10B"
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Pred. No. 1.03e-129;
0; Mismatches 9;
                                                                                                                                                                                                                                           vector to vector length is 146
Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                           /organism="Mus musculus"/strain="C57BL/6J"
                                                         Waterston, R.
The WashU-HHMI Mouse EST Project
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92.58;
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Best Local Similarity 92.5%;
Matches 135; Conservative
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C
                                                                                  Unpublished (1996)
                                                                                                                                                                                                                                                                                 1..145
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REFERENCE
AUTHORS
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total mouse RNA [providedby Minoru Ko, Wayne State Univ.]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library wen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo." /clone="670668"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 taaaaaatattgctttaaccgacactgtaaatatttcagataaacattatattttgtat 119
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                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@vatson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@inage.llnl.gov) for further information. MGI:410372 Putative full length read vector to vector length is 146 Seq primer: -28ml3 rev2 ET from Amersham.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 120)
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1-145
Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson Waterston R.;
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51 A; 22 C; 19 G; 53 T; 0 other;
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/lab_host="DH10B"
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Larity 92.5%; Pred. No. 1.03e-129;
Conservative 0; Mismatches 9;
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0; Mismatches
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                                                                                                     Contact: Wilson RK
WashU-Merck EST Project
WashU-Merck EST Project
WashU-Merck EST Project
WashU-Merck EST Project
WashU-Merch University School of Medicine
WashIngton University School of School of St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28MI3 rev2 from Amersham
High quality sequence stop: 67.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 TCTCCGCGCCCCAGCCGCCGGCTGCCAGCTTTTCGGGCCCCCGAGTCGCACCCAGCGAAG 167
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashD-Merck EST Project Unpublished (1995)
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Pred. No. 7.12e-86;
0; Mismatches 11; Indels
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/organism="Homo sapiens"
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Best Local Similarity 89.3%;
Matches 108; Conservative
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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521 CGGACACCAAGAAGTICCTGTGCTCGCTCTTCGCCCCCGGTCTGCCTCGATGACCTAGACG 580
                                           619 agcogotgocgocotgocgotoggtgtgogagogocoaaggocggotgotogocgotga 678
                                                                   679 tgogccagtacggcttcgcctggcccgagcgtgagctgcgaccgcctccc 730
                                                                                                                                                                     641 TGTCCGCCTTCGGCTTCCCCTGGCCCGACATGCTTGAGTGCGACCGTTTCCC 692
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AUTHORS
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                                                                                                                                                                                                                                    Human putative transmembrane receptor (frizzled 5) mRNA, complete
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                                         1999 TACTITACCTITAAAAGTICIAAAAATATIGCITITAACCAACACIGIAAAIATITICAGAI 1958
    Glibert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J. A large family of putative transmembrane receptors homologous the product of the Drosophila tissue polarity gene frizzled J. Biol. Chem. 271 (8), 4468-4476 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2334)
Wang, Y., Macke, J.P., Abella, B.S., Andreasson, K., Worley, P.,
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Abella, B., Wang, Y., Macke, J.P. and Nathans, J.
Direct Submission
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AUTHORS
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JOURNAL
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24-FEB-1996

800

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2421 bp

LCTVVFLLYYFFGMASSIWWYLİSLIWFLAAGMKWGNEALAGTSQYFHLAAWLVPSVK SIAVLALSSYDGDPVAGITYGNGSLDNIKGFYTAPLYTIFTĞGWFLAGFYSLFRI RSYIKQQGGFTKTHLEKLMIRLGLEFVLYYVPAAVVVACLEFEDHRREWEATHNCP CLRDLQPDQARREDYAVFMLKYFMCLVVGITSGVWWSGKTLESWRALCTRCCMASKG /product="transmembrane receptor" /db\_xref="PID:g1151260" /translation="MEWGYLLEVTSLLAALAVLQRSSGAAAASAKELACQEITVPLCK GIGYNYTYMPNOFNHDTQDEAGLEVHQFWPLVEIQCSPDLKFFLCSMYTPICLEDYKK PLPPCRSVCERAKAGCAPLMRQYGFAWPDRMRCDRLPEQGNPDTLCMDYNRTDLFTAA PSPPRRLPPPPPGEQPPSGSGHSRPPGARPPHRGGSSRGSGDAAAAPPSRGGKARPP vacsggapgaggrggaggaaaagagaagrgasspgargeyeelgaveqhvryeitgpa gggaapcepgcorapmysvsserhplynrvktgqiancalpchnpffsqderaftvf **AAVGAGAGGSGPGGSGPGPGGGGGGGGSLYSDVSTGLTWRSGTASSVSYPKQMPL** WIGLWSVLCFVSTFATVSTFLIDMERFKYPERPIIFLSACYLFVSVGYLVRLVAGHER Wang, Y., Macke, J.P., Abella, B.S., Andreasson, K., Worley, P., Gilbert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J. A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled J. Biol. Chem. 271 (8), 4468-4476 (1996) Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205 /note="putative transmembrane receptor" (bases 1 to 2421)
 Abella, B., Wang, Y., Macke, J.P. and Nathans, J.
 Direct Submission /map-"between Tp12 and Cdh2" 467 t /organism-"Mus musculus" Location/Qualifiers 779 g /gene="frizzled 8" /codon\_start=1 chromosome="18" 772 C 403 a source BASE COUNT JOURNAL CDS FEATURES

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CDS

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GNONLNSLRREVLGPLVIJLLVGTLELLAGEVSLERIRSVIKQGGTKTDKLEKLMIRI GIETLLYTVPASIVVACYLYEQHYRESWEAALJCACPGHDJGQPRAKPEYWYLMLKYF MCLVVGIJSGVWIWSGKIVESWRRFTSRCCCRPRRGHKSGGAMAAGDYPEASAALJGR

439 t

736 g

803 C

BASE COUNT

TGPPGPAATYHKQVSLSHV"

0; Gaps Score 56; DB 87; Length 2421; Pred. No. 1.17e-17; 0; Mismatches 121; Indels Query Match 2.8%; Best Local Similarity 59.4%; 177; Conservative Query Match Matches ORIGIN

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0; Mismatches 117; Indels 0; Gaps

Length 2334;

Score 58; DB 77; I Pred. No. 5.31e-19;

Query Match
Best Local Similarity 59.9%;
Matches 175; Conservative

499 aggargaggcgggcctggaggtgcaccagttctggccgctggtggagatccaatgctcgc 558

461 IGAAGGAGGIGCIGGAGGAGGCGGGGGGTIGGAICCCGGIGGICAIGAAGGAGGGGGGCACC 520 

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439 tgtgccggggatcgtcgacttgacgcacatgcccaaccagttcaaccacgacacgc 498

401 TGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCCAACCTGCTGGGCCACGAGACCA 460

306 tgccgttgtgcaaaggcatcggttacaactacacttadatgcccaaccagttcaaccacg 365 ö

366 abacgcaagatgaggcgggctagaggtgcaccagttttggccgctggtggdgatacagt 425

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Chan,S.D.H., Karpf.D.B., Fowlkes,M.E., Hooks,M., Bradley,M.S.,
Vuong,V., Bambino,T., Liu,M.Y.C., Arnaud,C.D., Strewler,G.J. and
Nissenson,R.A. Rattus norvegicus Drosophila polarity gene (frizzled) homologue Two homologs of the Drosophila polarity gene frizzled (fz) are widely expressed in mammalian tissues
J. Biol. Chem. 267, 25202-25207 (1992) cccgctggtgabggbgcagtgctc 347 GGGCACGAGAC 458 AFGARGCAGTGCCA 518 455 AGACCATGAAGGAGGTGCTGGAGCAGGCGGGGGGGTTGGATCCCGGTGGTGAAGCAGT 514 frizzled gene; homologue; polarity gene. Rattus jorvegicus (strain Sprague-Dawley) osteosarcoma cDNA to /note-"Drosophila polarity gene (frizzled) homologue" ac¢at¢atgeceaacettettgggeacaegaa 287 cccatctgcctggaggact 485 515 eccaccesaraccanaqapricererectederdindecdecesierecerdeareace 574 pacadeacaccardeaccarrecercecrecetecatecatereaaccecrecece 634 546 cgéteatgegedagtacggetttgettggeetgacggatgégetgegateggttgee 603 635 cégrcargrecécepreserredecresecesacarécrisasreses 692 ñ Length 1912; Mişmatches 114; Indels! CTGCCCAACCTGC DB 90; L Cacg /organism="Rattus norvegicus" /tissue\_type="osteosarcoma" 385 t geteeceggaceteaagtuetttetgtgtagaatg /strain="Sprague-Dawley /cell\_line="UMR106-01" /cell\_type-"osteoblast" Score 45; Pred. No. Socation/Qualifiers ה 566 /codon\_start=1 getgtgcacdgacategeetacaa 2.28; 662 c Best Local Similarity 60.2%; Matches 177; Conservative Rattus norvegicus Murinae; Rattus. ccdagaggadgcgg 399 GCTGTGCCAQ 299 GAAGGA mRNA, c Query Match source DEFINITION 288 ORGANISM BASE COUNT 228 REFERENCE AUTHORS 426 486 575 MEDLINE ACCESSION JOURNAL Ses KEYWORDS TITLE ORIGIN SOURCE g 윱 ò ö 용 ö გ

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PALLTTAPPPGLQFGAGTFGGPGGGGAPPRYATLEHFHCFRVLKVESTLSKELGE RDCAAPCEPARPDGSNEFSOEETRFARLMILTWSVLCCASTFFTVTTYLVDMORFRYP ERPIIFLSGCYTMVSVAXIAGFVLQERVVCNERFSEDGYRTVVQGTKREGCTILFMML YFFSMASSIWWVILSLTWFLAAGMKWGHEAIEANSQYFHLAAWAVPAVKTITILAMGO IDGDLLSGVCFVGLNSLDPLRGFVLAPLFVYLFIGTSFLLAGFYSLFRKTINKHDGT zhao,z., Lee,C.C., Baldini,A. and Caskey,C.T.
A human homologue of the Drosophila polarity gene frizzled has been
identified and mapped to 17q21.1
Genomics 27 (2), 370-373 (1995) KTEKLERLMYRIGVESYLYTVPATIVIACYFYEQAFREHWERSWYSQHCKSLAIPCPA HYTPRMSPDFTVYMIKYLMTLIVGITSGFWINSGKTLHSWRKFYTRLINSRHGETTV\* ä 327 ccaggaggacgcaggcctagaggtgcaccagttctatccgctggtgaaggtgcagtgctc 386 459 CATGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCA 518 267 getgtgeacggacatcgcctacaaccagaccatcatgcccaaccttctgggccacacgaa 326 399 GCTGTGCCACGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGAC 458 387 geoegaactgegettettetgtgeteeatgtaageaceegtgtgeaceg.tg--ctgga 443 519 cccesacaccaagaagriccrerecrecrerrescecececererecresarga 578 503 404 egdt 464 CGGT 638 24-MAY-1996 Pred. No. 4.63e-08; 0; Mismatches 116; Indels 3; Gaps Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1923)
Zhao, Z., Lee, C.C., Baldini, A. and Caskey, C.T. 444 acaggocatecogcogtgoogctatctgtgagogogogogogogggtgggaagcct gtqtgca-cggtg--ctgga recetesatsap CGTTTCCC ractacga cattteed Length 1923; Human frizzled gene product mRNA, complete cds. L37882 ACTGCGAC popo /note-"polarity gene; putative" DB 80; acgegeg 356 t /organism-"Homo sapiens" unction-"development" Score 41; ¢dagaccarccaccarccacrcdcrcrcc /tissue\_type="ovary"/chromosome="17" rizzled gene; polarity gene Location/Qualiflers 1..1923 639 CATGICCCCTICGCCTICCCCTGGCCCGA 590 9 /clone\_lib="fz-2" GFICCIGIGCIC /gene="frizzled" /map-"17q21.1" 133..1830 2.0%; Best Local Similarity 59.5%; Matches 175; Conservative ttoggettecag 671 c 96044450 306 g736678 uman. 465 catga SOURCE 'n source BASE COUNT ORIGIN DEFINITION REFERENCE AUTHORS 579 519 405 MEDLINE ACCESSION JOURNAL KEYWORDS CDS FEATURES TITLE RESULT ద ð å 셤 ä 유 à გ ö ö

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm

MPerch\_nn

Tue Dec 9 08:30:17 1997; MasPar time 741.29 Seconds 1311.186 Million cell updates/sec Run on:

Tabular output not generated.

>848439-2-trans Title:

(1-885) from translate seq 734 Perfect Score: Description:

1 ATGYINCARGGNCCNGGNWS.....SNATNMGNAARYINCARIGY 885 TACRANGTYCCNGGNCCNSW..........WNTANKCNTTYRANGTYACR N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch 362067 seqs, 549138275 bases x 2 Searched:

Minimum Match 0% Post-processing:

Listing first 45 summaries

embl-new3 Database:

1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORC 10:MAM 11:VRT 12:PLN 13:PR0 14:ROD 15:SYN 16:UNC

genbank99 17:VIR Database:

genbank-new3 105:VRL10

Database

106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV 112:MAM 113:VRT 114:PHG 115:PLN 116:PR11 117:PR12 118:ROD 119:SYN 120:UNA 121:VRL u-emb150\_99 122:part1

Database:

Dec 9 09:05

848439-2-trans.rge

Mean 15.331; Variance 11.948; scale 1.283 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	c	Query			4		2
No.	score	Match	Length	3	ID	Description	Fred, No.
-	720	98.1	1776	85	D50462	Mouse SDF5 mRNA, comp	0,00e+00
2	8	12.1		87	332	sculus puta	.25e-
m	75		2334	-	HSU43318	n putative t	6e-1
4	64	8.7	1770		CEU43316	Caenorhabditis elegan	2.45e-11
S	63		2831	83	MMU43317	Mus musculus putative	
9		8.3	2085	_	DMU 65589	Drogophila melanogast	75e-1
7	59		26		MMU45320	Mrs musculus putative	,36e-0
œ	26		1913		CEU 63557	orhabditi	.05e-0
6	26		4540		RATERZZH	Rattus norvegicus Dro	6.05e - 08
10	54		1923		HUMFRIZ	Human frizzled gene p	4.04e-07
11	52	-	1912	90	RATFRZH	us Dr	.64e-0
12	52	7.1	34576	00	CET 23D8		2.64e - 06
13	25	7.1	34576		CET 23D8	Caenorhabditis elegan	2.64e
14	52		34576		CET23D8	ditia	
c 15	49		215		128278	from	4
16	47	6.4	215	21	128278	Sequence 5 from paten	2.54e - 04
17	46		2624		MMU43205	lus fri	6.19e - 04
18	44	6.0	354		OFU89259	fallax 5	m
19	44	•	354		OFU89259	fallax	
	43		354	-	OFU89259	a fallax	ထ
c 21	43				OFU89259	fallax 57	8.51e-03
	36	5.3	74911	33	HS209H1		2.45e-01
	38		370		OFU89262	fallax 5	ш,
	88		370	Ξ	OFU89262	ı fallax 57	•
25	37		1509		æ	Insertion sequence IS	•
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27	37		1518		INSCDLA	Insertion sequence IS	1.23e+00
58	37		2187	4	PFAHSP70H	Plasmodium falciparum	
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30	36	4.9	2492	81	MMU43319	ξ.	2.70e+00
c 31	36		140571	34	HS46H23	A sequence *	•
32	32	•	1291	1	×		œ
33	35	•	1291	113		Xenopus laevis Frzb p	s,
34	ĭΣ	•	1875		XLU 68059		
32	32	•	4284	24	MHVLE N3C		5.86e+00
36	32	•	33200		CEF54B3	Caenorhabditis elegan	
37	32	•	47745		CET26E3	*** SEQUENCING IN PRO	œ
38	34	•	294	83	HUMUT612B		:22
39	34		41	44	PFU17812	laneta fuligino	~
40	34	4.6	9	33	DDU 67923	ictyostelium c	~
4	34	•	3618	38	CEZYG11	chabditis	2
c 42	34	•	4413	69	YSPCRM1N1	Yeast crml-N1 gene fo	2
43	34	4.6	13815	88	MUSDYSA	cophin mRN	26
44	34	4.6	34731	78	HSU75931		1.25e+01

## ALI GNMENTS

1	D50462 1776 bp mRNA	ION Mouse SDF5 mRNA, complete cds.
RESULT	LOCUS	DEFINITION

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Fax:81-75-753-4387, 2 (bases 1 to 175) Fax:81-75-753-4377, 2 (bases 1 to 176) Shirozu, M., Tada, H., Nakamura, T., Nelson, L.D., Martina, N., Hamada, T., Sato, T., Tashiro, K., Nakano, T. and Honjo, T. Isolation of novel genes encoding for escreted or membrane proteins using signal sequence trap Unpublished (1995) /translation="MPRGPASLLLLVLASHCCLGSARGLFLFGQPDFSYKRSNCKPIP **ANLQLCHGIEYQNMRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPV** CLDDLDETIQPCHSLCMQVKDRCAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDH LLPATEEAPKVCEACKTKNEDDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKS KTIYKLNGVSERDIKKSVLMIKDSLQCTCEEWNDINAPYLVMGQKQGGELVITSVKRM Submitted (01-MAY-1995) to the DDBJ/EMBL/GenBank databases. Michio Mus musculus cell line:ST-2 cDNA to mRNA, clone\_lib:phage (lgt22a) library, ST-2 directional 1. Shirozu, M., Tada, H., Tashiro, K., Nakamura, T., Lopez, N.D., Nazarea, M., Hamada, T., Sato, T., Nakano, T. and Honjo, T. Characterization of novel secreted and membrane proteins isolated ö /cell\_line="ST-2" /clone\_lib="phage (lgt22a) library, ST-2 directional 1" 14..901 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciuroynathi; Muridae; Murinae; 134 aagcccatccccgccaacctgcagctgtgccacggcatcgagtaccayuacatgcggctg 193 74 teggegegtgggetetteetetteggeeageeegactteteetaeaagegeageaactge 133 Shirozu, Kyoto University, Faculty of Medicine, Department of Medical Chemistry; Yoshida, Sakyo-ku, Kyoto, Kyoto 606, Japan (E-mail:kondo@virusl.virus.kyoto-v.ac.jp, Tel:81-75-753-4377, Gaps ö ch 98.1%; Score 720; DB 85; Length 1776; 1 Similarity 58.1%; Pred. No. 0.00e+00; 514; Conservative 213; Mismatches 158; Indels 0 /gene="SDF5" 455 t by the signal sequence trap method Genomics 37 (3), 273-280 (1996) 97092876 /organism="Mus musculus" /codon\_start=1 /db\_xref="PID:g1747302" QKGQREFKRISRSIRKLQC" 405 g Location/Qualifiers (bases 1 to 1776) 483 c Direct Submission Mus musculus Best Local Similarity Shirozu, M. (sites) g1747301 SDF5. 433 Mus. Query Match source ORGANISM BASE COUNT TITLE JOURNAL Matches ACCESSION REFERENCE AUTHORS REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS JOURNAL KEYWORDS CDS TITLE TITLE SOURCE ORIGIN 음 용 셤 à 8 ð

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194	254	314	301	374	361	434	17.	494	554	541	614	691	674	661	734	721	794	781	854	841	Ē	ACCESSION	ORDS	ORGANISM	ERENCE	
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TITLE JOURNAL AUTHORS

REFERENCE JOURNAL

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A large family of putative transmembrane receptors homologous to

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CYLCVSLGFLVRLVVGHASVACSREHNHIHYETTGPALCTIVFLLVYFFGMASSIWWV ILSLTWFLAAAMKWGNEXIAGYGQYFHLAAWLIPSVKSITALALSSVDGDPVAGICYV GYNLTHMPNOFNHDTQDEAGLEVHQFWPLVETQCSPDLRFFLCTMYTPICLPDYHKPL PPCRSVCERAKAGCSPLMRQYGFAWPERMSCDRLPVLGRDAEVLCMDYNRSEATTAPP RPFPAKPTLPGPPGAPASGGECPAGGPFVCKCREPFVPILKESHPLYNKVRTGQVPNC **AVPCYQPSFSADERTFATFWIGLMSVLCFISTSTTVATFLIDMDTFRYPERPIIFLSA** GIFTLLYTVPASIVVACYLYEQHYRESWEAALTCACPGHDTGQPRAKPEYWVLMLKYF GNONINSLRRFVLGPLVLYLLVGTLFLLAGFVSLFRIRSVIKQGGTKTDKLEKLMIRI MCLVVGITSGVWIWSGKTVESWRRFTSRCCCRPRRGHKSGCAMAAGDYPEASAALTGR /translation="MARPDPSAPPSLLLLLLAQLVGRAAAASKAPVCQEITVPMCRG HSU43318 2334 bp mRNA PRI 24-FEB-1996 Human putative transmembrane receptor (frizzled 5) mRNA, complete Wang, Y., Macke, J.P., Abella, B.S., Andreasson, K., Worley, P., Cilbert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J. A large family of putative transmembrane receptors homologous the product of the Drosophila tissue polarity gene frizzled J. Biol. Chem. 271 (8), 4468-4476 (1996) 439 tgtgccgcggcatcggctacaacctgacgcacatgcccaaccagttcaaccacgacacgc 498 499 aggacgaggcgggcctggaggtgcaccagttctggccgctggtggagatccaatgctcgc 558 146 INTGYCAYGGNAINGARTAYCARAYAIGMGNYINCCNAAYYINYINGGNCAYGARACNA 205 206 TGAARGARGTNYINGARCARGCNGGNGCNTGGAINCCNYINGINATGAARCARIGYCAYC 265 Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; 44; Mismatches 132; Indels /note="putative transmembrane receptor" Abella, B., Wang, Y., Macke, J.P. and Nathans, J. Direct Submission /product="transmembrane receptor" Score 75; DB 77; Pred. No. 3.36e-16; 439 t /organism="Homo sapiens" /db\_xref="PID:g1151252" /tissue\_type="retina" 321..2078 FGPPGPAATYHKQVSLSHV" 736 g Location/Qualifiers /gene="frizzled 5" /chromosome="2' /map="2q33-34" /codon start=1 (bases 1 to 2334) (bases 1 to 2334) Query Match 10.2%; Best Local Similarity 39.7%; Matches 116; Conservative 803 c Baltimore, MD 21205 1..2334 355.4 Homo sapiens g1151251 043318 human. m source DEFINITION ORGANISM BASE COUNT ACCESSION AUTHORS AUTHORS JOURNAL REFERENCE MEDLINE REFERENCE JOURNAL KEYWORDS CDS FEATURES TITLE TITLE SOURCE ORIGIN g ò g ð /product="transmembrane receptor" /db\_xref="PID:g1151260" /translation="MEMCYLLEVTSLIAALAVLQRSSGAAAASAKELACQEITVPLCK RSVIKQQGGPTKTHKLEKLMIRLGLFTVLYTVPAAVVVACLFYEQHNRPRHFATHNCP CLRDLQPDQARRPDYAVFMLKYFMCLVVGITSGVWVWSGKTLESWRALCTRCCHASKG PLP PCRSVCERAKAGCAP LMRQYGFAWPDRMRCDRLPEQGNPDTLCMDYNRTDLTTAA PSPPRRLPPPPPGEQPPSGSGHSRPPGARPPHRGGSSRGSGDAAAAPPSRGGKARPP VACSGGAPGAGGRGGAGGAAAGAGAAGRGASSPGARGEYEELGAVEQHVRYETTGPA **LCTVVFLLVYFFGMASSIWWVILSLTWFLAAGMKWGNEAIAGYSQYFHLAAWLVPSVK** SIAVLALSSVDGDPVAGICYVGNQSLDNLRGFVLAPLVIYLFIGTMFLLAGFVSLFRI GIGYNYTYMPNQFNHDTQDEAGLEVHQFWPLVE1QCSPDLKFFLCSMYTPICLEDYKK GGGAAPCEPGCQCRAPMVSVSSERHPLYNRVKTGQIANCALPCHNPFFSQDERAFTVF WIGLMSVLCFVSTFATVSTFLIDMERFKYPERPIIFLSACYLFVSVGYLVRLVAGHEK **AAVGAGAGGSGPGGGGGGGGGGGGGSLYSDVSTGLTWRSGTASSVSYPKQMP**I ö 366 acacgcaagatgaggcgggcctagaggtgcaccagttttggccgctgy.ggagatacagt 425 gctcccggacctcaagttctttctgtgtagcatgtacacycccatctgcctggaggact 485 320 TNGAYGARACNATNCARCCNTGYCAYFINYTHTGYGTNCARGTNAARGAYMGNTGYGCNC 379 200 ARACNATGAARGARGTNYTNGARCARGCNGGNGCNTGGATNCCNYTNGTNATGAARCART 259 260 GYCAYCCNGAYACNAARAARTTYYTNTGYWSNYTNTTYGCNCCNGTNTGYYTNGAYGAYY 319 486 acaagaagcetetgecgeettgtegetetgtgtgtgaacgegecaaggeeggetgegege 545 546 egeteatgegecagtacggetttgettggectgacegeatgegetgegateggttgeegg 605 Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Gaps the product of the Drosophila tissue polarity gene frizzled J. Biol. Chem. 271 (8), 4468-4476 (1996) .**.** Score 89; DB 87; Length 2421; 47; Mismatches 131; Indels /note="putative transmembrane receptor" 2 (bases 1 to 2421)
Abella,B., Wang,Y., Macke,J.P. and Nathans,J.
Direct Submission Pred. No. 1.25e-22; /map="between Tpl2 and Cdh2" 467 t /organism="Mus musculus" Location/Qualifiers 6 /gene="frizzled 8" 179 /chromosome="18" <u>::</u> /codon\_start=1 Query Match 12.1%; Best Local Similarity 41.1%; Matches 124; Conservative 772 c Baltimore, MD 21205 1..2421

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0у 386	TGMSNGCNTTYGGNTTYCCNTGGCGNGAYATGYTNGARTGYGAYMGNTTYCC 437	qq	265	265 tctgctccga
RESULT	4	δy	257	257 ARTGYCAYCC
TION		ΩP	325	aactagccaa   :    :
ACCESSION	gene, complete cds. U43316	ò	317	317 AYYTNGAYGA
NID KEYWORDS	g1151249	qq	385	385 ttccagtgct 
SOURCE ORGANISM		δ	377	377 CNCCNGTNAT
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;	qq	445	445 cgttggagaa   :
บบบบบบบบบ	Rhabditidae, Caenorhabditis.	Qy	437	437 CNCARGAYAA
AUTHORS	Wang, Y., Macke, J.P., Abella, B.S., Andreasson, K., Worley, P.,	ţ		u
TITLE	<pre>Gilbert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J. A large family of putative transmembrane receptors homologous to</pre>	KESULT LOCUS		n
JOSTRNAT	the product of the Drosophila tissue polarity gene frizzled	DEFI	DEFINITION	Mus musc
MEDLINE	9. 5224032	ACCE	ACCESSION	043317
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TITLE	Direct Submission	SOURCE	SCE.	
JOURNAL	Submitted (14-DEC-1995) Jèremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street,	NO.	ORGANISM	
FEATURES	Baltimore, MD 21205 Location/Qualifiers			Vertebra Murinae;
source		REFE AU	REFERENCE AUTHORS	<pre>1 (base Wang,Y.,</pre>
	/chromosome="I"	Ē	1919	Gilbert,
CDS	/map="on IACE 19388 and 134D9" 57,.1634	7	3	the prod
	/gene="frizzled 1" //orbowles 1. mushting transmemberns reconter"	S M	JOURNAL MEDITAL	J. Biol.
	/ince= 12 1; purative transmembiane receptor /codon start=1	REFE	REFERENCE	2 (base
	/product="transmembrane receptor"	AU	AUTHORS TITIE	Abella, B
	/translation="MGFFGYLGVTWLLLEVICVDGQRCQKVDHEMCNDLPYNLTSF	90	JOURNAL	Submitte
	PNLVDEESWRDASES1LITYRELLSVVCSEQLKFFICSVTFPMCNEKLANFIGPCKFLLC LSVQEKCLPVLESFCFKWPDVIRCDKFPIENNREKMOMKGPNEQCAIQDERAKFPAKE			Genetics Baltimor
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Query Ma	Query Match 8.7%; Score 64; DB 38; Length 1770;			
Best Loc	al Similarity 37.5%; Pred. No. 2.45e-11;			

Macke, J.P., Abella, B.S., Andreasson, K., Worley, P., t.D.J., Copeland, N.C., Jenkins, N.A. and Nathans, J. e family of putative transmembrane receptors homologous to oduct of the Drosophila tissue polarity gene frizzled 1. Chem. 271 (8), 4468-4476 (1996) ata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; 17 2831 bp mPNA ROD 24-FEB-1996 sculus putative transmembrare receptor (frizzled 4) mRNA, ggaaagacgcctccgaatccatcacctacaagcccctgctctccgttg 264 agcageteaaattetteetgtgeteegtetaetteeegatgtgeaaegaga 324 CONGAYACNAARAARTTYYTNTGYMSNYTNTTYGCNCCNGTNTGYYTNGAYG 316 acceattggtccatgccgtccattgtgtctttccgtccaggaaaagtgtc 384 tgtgcaacgatttgccgtataacttaacgagcttcccaaatctcgtcgacg 204 ed (14-DEC-1995) Jeremy Nathans, Molecular Biology and is, Johns Hopkins Medical School, 725 N. Wolfe Street, Gaps tae; mitochondrial eukaryotes; Metazoa; Chordata; ö Indels es 1 to 2831)
B., Wang,Y., Macke,J.P. and Nathans,J.
Submission 848439-2-trans.rge 47; 'Yismatches 150; Location/Qualifiers es 1 to 2831) re, MD 21205 onservative acaatc 459 AYGAYY 451 . Wus. e cds. sculus Dec 9 09:05

/product="transmembrane receptor" /db\_xref="P1D:g1151254" /translation="MAWPGTGPSSRGAPGGVGLRLGLLLQFLLLLRPTLGFGDEEERR

/note="putative transmembrane receptor"

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CDS

GEGDEVPLPHKTP IQPGEECHSVGSNSDQY IWVKRS LNCVIKCCYDAĞLYSRSAKEF
TDI MMAWASICFISTTETULTFILDSRFS YPERP ITFLSMCYNIYSIAY IVETU TDI MMAWASICFISTTETULTFILDSRFS YPERP ITFLSMCYNIYILTWETANGY WGREN ISODFEEAMEVULODGLINYTOGAL ITFLLMYFFGGMASSIWWY LILTWFLAACLK WGREN ISODFEEN SYFELIAMAN INTULMELUNDBELITGLYVGNQULDALTGEV VIACYFYELSNWALFRYSADDSNMAVEMIK IFMS LLVGITSGWHIWSAKTIHTWQKCS **VPMCTEKINIPIGPCGGMCLSVKRRCEPVLREFGFAWPDTLNCSKFPPQNDHNHMCME** ODP IRTAMCONLGYNVTKMPNLVGHELQTDAELQLTTFTPLIQYGCSSQLQFFLCSVY

3 others NRLVNSGKVKREKRGNGWVKPGKGNETVV" 725 t 711 g 703 c 689 BASE COUNT

ORIGIN

ö Gaps ö Score 63; DB 87; Length 2831; Pred. No. 6.61e-11; 40; Mismatches 127; Indols Query Match 8.6%; Best Local Similarity 38.8%; 106; Conservative Query Match Matches

tgcccaacttagtgggacacgagctgcagacagacgccgagctgcagctgacaactttca 574 179 TNCCNAAYYTNYTNGGNCAYGARACNATGAARGARGTNYTNGARCARGCNGGNGCNTGGA 238 = :: :: :: 515 임 ð

634 575 egcegeteatecagtacggetgetceagecagetgeagttetteetttgtteggtttatg 셤

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695 cagtcaagagacgetgtgaaccagteetgagagaatttgggtttgeetggeeegaeaeee 754

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755 tgaactgcagcaagttcccgccccagaacgacc 787 ð

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Bhanot, P., Wang, Y. and Nathans, J.
Direct Submission
Submitted (30-JUL-1996) Molecular Biology and Genetics, Johns
Hopkins University School of Medicine, 725 N. Wolfe St., 805 PCTB, Bhanot, P., Brink, M., Samos, C.H., Hsieh, J.C., Wang, Y., Macke, J.P., Andrew, D., Nathans, J. and Nusse, R. A new member of the frizzled family from Drosophila functions as 01-SEP-1996 Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 2085) Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; илиоээву 2085 bp DNA INV 01-SE Drosephila melanogaster Dfz2 (Dfz2) gene, complete cds. U65589 Nature 382 (6588), 225-230 (1996) Location/Qualifiers Baltimore, MD 21205, USA Drosophila melanogaster (bases 1 to 2085) Wingless receptor fruit fly. g1518050 9635397. ٩ DEFINITION ORGANISM TITLE JOURNAL ACCESSION AUTHORS REFERENCE MEDLINE REFERENCE AUTHORS JOURNAI KEYWORDS FEATURES TITLE SOURCE

GAGGSSGSTSTKPCRĆIVSKNONPQGEKASGKECSCSCRSPLIFLGKEQLLQQQSQM PMMHPHHYYMNLTVQRIAGVPNCLIPCKGPFFSNDEKDFAGLMIALMSGLCFCSTLM HSCTLVFLLTYFFGMASSIWWILTFTWFLAAGLKWGNEAITKHSQYFHLAAWLIPTV QSYAVLLLSAVDGDPILGICYVGNINPDHLKTFVLAPLEVYLVIGTTFLMAGFVSLFR PLVEIKCSPDLKFFLCSMYTPICLEDYHKPLPVCRSVCERARSGCAPIMOQYSFEWPE RMACEHLP LHGDPDNI, CMEQPSYTEAGSGGSSGGSGGSGSGGKRKQGGSGSGS IRSVIKQQGGVGAGVKADKLEKIMIRIGIFSVLYTVPATIVIGCYLYBAAYFEDWIKA LACPCAQVKGPGKKPLYSVLMIKYFMALAVGITSGVWIWSGKTLESWRRFWRRLLGAP /translation="MRHNRLKVLILGLVLLLTSCRADGPLHSADHGMGGMGMGGHGLD **ASPAPGYGVPAIPKDPNLRCEEITIPMCRGIGYNMTSFPNEMNHETQDEAGLEVHQFW TLTTFIIDTERFKYPERPIVFLSACYFMVAVGYLSRNFLQNEEIACDGLLLRESSTGP** DRTGANQALIKQRPPIPHPYAGSGMGMPVGSAAGSLLATPYTQAGGASVASTSHHHLH /note="Description: frizzled 2; wingless receptor' /standard\_name="frizzled2" /db xref="PID:q1518051" 'product="Dfz2" chromosome="3" /codon start=1 /gene="fz2" "map="76A" 1..2085

406 612 g HHVLKQPAASHV 663 c 404

BASE COUNT

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Gaps ö Length 2085 42; Mismatches 150; Indels Pred. No. 4.75e-10; Score 61; DB 40; Query Match 8.3%; Best Local Similarity 38.5%; 120; Conservative Matches

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206 taccaatgtgtcggggcattggctacaacatgacatccttccccaacgaaatgaaccatg 265 \_ :: g

140 INCARYTNIGYCAYGGNAINGARIAYCARAAYAIGMGNYINCCNAAYYINYINGGNCAYG 199 음 ð

266 agacccaggacgaagcgggcctggaggtgcaccagttctggcccctggtggagatcaaat 200 ARACNATGAARGARGINYINGARCARGCNGGNGCNIGGAINCCNYINGINAIGAARCARI ••• ð

385 326 getegeceggaceteaagttetteetgtgeageatgtacaegeceatetgeetggaggatt 염

260 GYGAYCCNGAYACNAARAARTTYYTNTGYWSNYTNTTYGCNCCNGTNTGYYTNGAYGAYY 319 ð 386 accacaagccgctgcccgtttgccggrgtgtctgcgagagagcccgctcgggatgcgcac 445 320 INGAYGARACNATNCARCCNTGYCAYWSNYTNTGYGTNCARGTNAARGAYMGNTGYGCNC 379 g ð

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506 ttcatggtgacc 517 쇰

440 ARGAYAAYGAYY 451 δ

MMU43320 2260 bp mRNA ROD 24-FEB-1996 Mus musculus putative transmembrane receptor (frizzled 7) mRNA, complete cds house mouse. g1151257 DEFINITION ORGANISM ACCESSION KEYWORDS RESULT LOCUS

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Mus musculus

/organism="Drosophila melanogaster"

source

Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;

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Wang, Y., Macke, J.P., Abella, B.S., Andreasson, K., Worley, P., Gilbert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J. A large family of putative transmembrane receptors homologous the product of the Drosophila tissue polarity gene frizzled J. Biol. Chem. 271 (8), 4468-4476 (1996) 522 tecegttgtgcaeggatategeetacaaecagaecateetgeeeaaeetgetgggeeaea 581 641 200 ARACNATGAARGARGTNYTNGARCARGCNGGNGCNTGGATNCCNYTNGTNATGAARCART 259 642 gttctcctgagctacgcttcttcttatgctctatgtacgcacccgtgtgcaccg-tg--c 698 Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Gaps 582 cgaaccaagagacgcgggcctcgaggtgcaccagttctaccctctggtaaaggtgcagt .; ; Score 59; DB 87; Length 2260; 44; Mismatches 133; Indels 1 others /note="putative transmembrane receptor" Abella, B., Wang, Y., Macke, J.P. and Nathans, J. /product="transmembrane receptor" Pred. No. 3.36e-09; 481 t /organism="Mus musculus" Location/Qualifiers 9 /gene="frizzled 7" 677 /chromosome="2 /map="2q33-34" 362..2080 /codon\_start=1 (bases 1 to 2260) 8.0%; Best Local Similarity 39.6%; Matches 118; Conservative 739 c Baltimore, MD 21205 Direct Submission 1..2260 Murinae; Mus. 96224032 Query Match source BASE COUNT AUTHORS AUTHORS JOURNAL REFERENCE MEDLINE REFERENCE JOURNAL CDS TITLE ORIGIN g g В ð S 유 8 셤 ð ð

Dec 9 (9):05 8/0439-2-trans.rge

ALESFLTFAIDRKRFRFPERCVFYLSLCIFISSLPYLTPLFIDAPIRSCHALGNGRSY LSICTFDNSYCLASFLLNYFFSTAAALWWLMFSFTLYLSGGRKWVPEGIEACSSYVHF VCEQVKADCFSILEEFGIGWPEPLNCAQFPDPPELCMKPTEDEITGGFSAPRLPTKGS GGFASMCRERISFRTRGTDTSKLEKLMVKMGFFCALFILDNVIELVCQCYKFMILTQM TRMTIDCKQQSGACHRPTPPQAEIYMTAVISSLATGFSCLMMVLSAKTVHAWKNFIFC YFPNTILHNDQHTLQTHTEHFKPLMKTKCHPHIHFFICSVFAPMCPIGMPQAVTSCKS SSSSSKPTGCPSDLVDVDPHDPKSHCAFACQSNVMFSTDNKRMVRSWS IWFAAANAGV VAWGLSSLATIIVLIFNKVDASELTALCSVGNLNSIALLWFVIVPRTICIVIGTCFIV translation="MMHSLGIILLFIPLATGSIFDQAVKGKCIPIDIELCKDLPYNY" Caenorhabditis elegans transmembrane receptor LIN-17 (lin-17) mRNA, :: /function="regulates certain asymmetric cell divisions" Sawa, H., Lobel, L. and Horvitz, H.R.
The Caenorhabditis elegans gene lin-17, which is required for certain asymmetric cell divisions, encodes a putative seven-transmembrane protein similar to the Drosophila frizzled 72 ttattccactcgccacaggatcaattttcgatcaggcggtgaaaggg-aaatgcattccg 130 131 atcgacattgagctatgcaaagacctgccctacaactacacatattcccgaataccatt 190 133 GCNAAYYTNCARYTNTGYCAYGGNATNGARTAYCARAAYATGMGNYTNCCNAAYYTNYTN 192 Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoldea; Submitted (11-JUL-1996) Biology, Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139, USA Gaps GMCSSAPVKNPIEPSTRPLLEPPTAPPPQPPVYMQMATNPQNSWRPSKVV' :: Length 1913; Indels /product="transmembrane receptor LIN-17" /note="similar to Drosophila Frizzled" ΙΝ /organism="Caenorhabditis elegans" 55; Mismatches 192; /note="SL1 trans-splice leader" Score 56; DB 38; Pred. No. 6.05e-08; Genes Dev. 10 (17), 2189-2197 (1996) 96397419 /db xref="PID:g1589780" Location/Qualifie:s 406 g Rhabditidae; Caenorhabditis. /chromosome="I" Sawa, H. and Horvitz, H.R. /gene="lin-17" /codon start=1 Caenorhabditis elegans. Caenorhabditis elegans /strain≈"N2" 1913 bp 1 (bases 1 to 1913) 7.68; (bases 1 to 1913) Best Local Similarity 35.8%; Matches 138; Conservative Direct Submission 41..1717 1..1913 1..10 complete cds. q1589779 CEU 63557 protein 466 misc\_feature Query Match œ source DEFINITION ORGANISM BASE COUNT ACCESSION JOURNAL REFERENCE AUTHORS MEDLINE AUTHORS JOURNAL REFERENCE KEYWORDS CDS TITLE TITLE ORIGIN 임 ð 셤 ð

848439-2-transinge 13	<ul> <li>191 ctacacaacgatcaacacgcttcaaacccacacggagicttcaagccgttgatgaaa 250</li> <li>193 GUNCAYGARACNATGAARGTNITHGARCARGCGNGCNTGGATNCCNYTHGTNATG 252</li> <li>251 acaaaaatgccatccaacattcacttcttcatttgctccqtttttgctccaatgtgcccg 310</li> </ul>	:  :  :    :     :      :    ::    :	attggaatgccacaggccgtgacaagctgcaatccgtttgcgagcaagtgaaagcggat 370 :	tgcttctcgatattggaagaattcgggattggatggccgagcgctgaattgtgcacaa 430   :	t 456 1 17 458	RATERZEH 4540 bp mRNA ROD 16-JUL-1993 RATERSZH GASTGUE ACTOR DESCRIPTION OF THE STATE OF THE STA	KEFLCSMYAPVCTVLEQALPPCRSLCERAĴGCEALMNKEGFOMPDTIKCEKFPVHGAG ELCVGQNTSDKGTPTFSLLPEFWTSNZQHGGGGTRGGYPGGAGPVERGKESCPRALRV PSYLNYHFLGEKDCGAPCEPTKYYGLMYFGPEELLRPSRTW1G1WSVLCCASTLFTVLI YLVDMRRFSYPERP IJELSGCYTAVANAYIAGFLLEDRVVCNDKFAEDGARTVAGGTK KEGCTILLFMLYFFSAISSTWWVILSTYFRAAGKKWGHFAIFANSQYFHLAAWAVPA
Dec 9 09:05 8484'	Db 191 ctacacaacgatcaacacacgcttcaaacc 	:  :  :  :    :        Qy 253 AARCARTGYCAYCONGAYACNAARAARITY	Db 311 attggaatgccacaggccgtgacaagctgc 1	Db 371 tgcttctcgatattggaagaattcgggatt	Db 431 ttcccagatccaccggagctttgcat 456	RESULT 9 RATFRZZH 4540 bp mRNA Battus norvegicus Drosophila polarity gen mRNA, complete cds.  ACCESSION NID FIZZLEd gene; homologue; polarity gene. SOURCE RATTUS norvegicus (strain Sprague-Dawl:y) RATTUS norvegicus (strain Sprague-Dawl:y) RATTUS norvegicus Eukaryotae; mitochondrial eukaryotes; Mei Vertebrata; Eutheria; Rodentia; Sciurogna Murinae; Rattus Nunnae; Rattus Nunnae; Rattus TITLE TYPEBRORO, TY, Liu, M.Y.C., Arnaud, Nunnay, Bambino, T., Liu, M.Y.C., Arnaud, Nunnay, Sababino, T., Liu, M.Y.C., Arnaud, Nunday expressed in mammalian tissues JOURNAL JOURNAL JOURNAL JOURNAL JOURNAL JOURNAL JOOGANISM SETTAIN="Sprague-Danity gene /cell_Type="osteosarcoma" /con_astart=1 /db_xref="plosgillation" /con_astart=1 /db_xref="osteosarcoma" /con_astart=1 /db_xref="plosgillation" /con_astart=1 /db_xref="plosgillation" /con_astart=1 /db_xref="plosgillation" /con_astart=1 /db_xref="plosgillation" /con_astart=1 /con_	KEFLCSMYAPVCTVLEQAL ELCVGQNTSDKGTPTPSLL PSYLNYHFLGEKDCGAPCE YLVDMRRFSYPERP ITFLS KEGCTILFMMLYFFSMASS IXTTITIALGANGENISS

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A human homologue of the Drosophila polarity gene frizzled has been identified and mapped to 17921.1 Genomics 27 (2), 370-373 (1995) 96044450 PAILITAPPPGLQPGAGGTPGGGGAPPRYATLEHPFHCPRULKVPSYLSYKFLGE RDCAAPCEPARPDGSMFFSQEETRFARLMILTWSVLCCASTFFTVTTYLVDMQRFRYP SCKSYAIPCPHLQCGCGVPPHPPMSPDFTVFMIKYLMTLIVCITSCFWIWSGKTLNSW RKFYTRLTNSKQGETTV" /translation="MRPRSALPRLLLPLLLPAAGPAQFHGEKGISIPDHGFCQPISI PlcTDlaynQTIMDNLLGHTNQEDAGLEVHQFYPLVKVQCSPELRFFLCSMYAPVCTV LEQAIPPCRSICERARQGCEALANKFGFOWPERLRCEHFPRHGAEQICVGONHSEDGA 4; 1112 tecegetytgeaeggaeategegtaeaateagaeeateatgeeeaaeetgetyggeeaea 1171 1290 -ggagcaggcgctgcctgccgctccctgtgcgagcgcgcccagg---gctgcgagg 1345 1172 cgaatcaggaggacgccggcctggaggtgcaccagttctacccgttggtgaaggtgcagt 1231 200 ARACNATGAARGARGTNYTNGARCARGCNGGNGCNTGGATNCCNYTNGTNATGAARCART 259 32) TIGAYGARACNATNCARCCNTGYCAYWSNYTNTGYGTNCARGTNAARGAYMGNTGYGCNC 379 1346 cactcatguacaagttcggcttccagtggccagacccgctcaagtgcgagaagttccc 1403 Gaps 24-MAY-1996 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; ; 9 Score 56; DB 90; Length 4540; Pred. No. 6.05e-08; 47; Mismatches 124; Indels HUMFRIZ 1923 bp mRNA PRI Human frizzled gene product mRNA, complete cds. L37882 Zhao, Z., Lee, C.C., Baldini, A. and Caskey, C.T. /note="polarity gene; putative" ų /organism="Homo sapiens" /function="development" /db\_xref="PID:g736679" /clone\_lib="fz-2" /tissue\_type="ovary" /chromosome="17" 1220 g frizzled gene; polarity gene. Location/Qualifiers /gene="frizzled" /map="17q21.1" 133..1830 /codon start=1 1923 bp Query Match 7.6%; Best Local Similarity 40.6%; 1 (bases 1 to 1923) 1255 c 121; Conservative 1..1923 Homo sapiens 993 a g736678 human. DEFINITION ACCESSION 10 BASE COUNT ORIGIN ORGANISM Matches REFERENCE AUTHORS MEDLINE JOURNAL CDS KEYWORDS TITLE 염 연 셤 g 염 ò ð ð ð ð

ERP I I FLSGCYTMVSVAY I AGFVLQERVVCNERF SEDGYRTVVQGTKKEGCT I LFWMLYF SMASS I WWVI LS LTWF LAAGMKWGHEA I EANSQYF HLAAMAVPAVKT I TI LAMGQ I DGDLLSGVCFVGLNSLDP LRGFVI AP LFVYLF I GTSF I LAGFVSLFRI RT I MKHDGT KTEKLERLMVR I GVFSVLYTVPATI VI AGYFYEQAFREHWERSWYSQHCKSLA I PCPA HYTPRMSPDFTVYMIKYLMTLIVGITSGFWIWSGKTLHSWRKFYTRLTNSRHGETTV" 671 c 590 q 356 t

590 g æ 306 BASE COUNT

ORIGIN

; Gaps 3; Length 1923; 41; Mismatches 137; Indels Score 54; DB 80; Pred. No. 4.04e-07; DB 80; Query Match 7.4%; Best Local Similarity 39.7%; 119; Conservative Matches tecegetgtgcaeggacategectacaaecagaceateatgeecaaeettetgygeeaca 322 <del>..</del> <u>::</u> = 263 음 à

140 INCARYINTGYCAYGGNATNGARTAYCARAAYATGMGNYT ICCNAAYYTNYTNGGNCAYG 199

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380

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RATFRZH 1912 bp mRNA ROD 16-JUL-1993 Rattus norvegicus Drosophila polarity gene (frizzled) homologue complete cds. g310114 mRNA. DEFINITION ACCESS 10N LOCUS

Rattus norvegicus (strain Sprague-Dawley) osteosarcoma cDNA mRNA. KEYWORDS SOURCE

frizzled gene; homologue; polarity gene.

Rattus norvegicus ORGANISM

Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Murinae; Rattus

1 (bases 1 to 1912) Chan, S.D.H., Karpf, D.B., Fowlkes, M.E., Hooks, M., Bradley, M.S., Vuong, V., Bambino, T., Liu, M.Y.C., Arnaud, C.D., Strewler, G.J. and Two homologs of the Drosophila polarity gene frizzled (fz) are Nissenson, R.A. REFERENCE AUTHORS TITLE

widely expressed in mammalian tissues J. Biol. Chem. 267, 25202-25207 (1992) 93094228 JOURNAL MEDLINE

Location/Qualifiers

FEATURES

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xref="PID:g310115"

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566 g U 662 æ 299

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BASE COUNT

ORIGIN

DB 90; Length 1912; Pred. No. 2.64e-06; Score 52; Best Local Similarity 39.3%; Query Match

2; Caps 3; 41; Mismatches 138; Indels 118; Conservative

224 tecegetgtgeaeggaeategeetaeaaceagaeeateatgeeeaaeettettgggeaea 283

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343 cgaaccaagaggacgcgggcctggaggtgcatcaattctacccgctggtgaaggtgcagt 284

259 200 ARACNATGAARGARGINYINGARCARGCNGGNGCNTGGATNCCNYTNGTNATGAARCART gotogocogagotgogottottoctgtgotocoatgtacgotocoggtgtgcacgg-tg--c 400 344

319 GYCAYCCNGAYACNAARAARTTYYTNTGYWSNYTNTTYGCNCCNGTNTGYYTNGAYGAYY 260

401 tggagcaggccatcccgccgtgccgctccatctgcgaacgcgcgcccaaggctgcgagg 460 g

320 INGAYGARACNATNCARCCNTGYCAY#SNYTNTGYGTNCARGTNAARGAYMGNTGYGCNC 379 ð

461 egetcatgaacaagtteggetteeagtggeeegagegeeteegetgegageattteeege 520 g

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standard; DNA; INV; 34576 LT 12 CET23D8 281128;

e1008304

21-OCT-1996 (Rel. 49, Created) 01-MAR-1997 (Rel. 51, Last updated,

Version 5)

Caenorhabditis elegans cosmid T23D8 

CD63 antigen like; Drosophila tissue polarity protein like; histone H2A; histone H4; Mouse bright protein like;

protein. transporter

Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Caenorhabditis elegans

Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;

Peloderinae; Caenorhabditis. Rhabditidae;

1-34576

Wild A.;

Submitted (21-0CT-1996) to the EMBL/GenBank/DDBJ databases.
Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or

rw@nematode.wustl.edu
[2]

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MEDLINE; 94150718.

Nature 368:32-38(1994)

C. elegans'

IMPORTANT:

Location/Qualifiers

sequence CET24D1.

source

'product="T23D8.8"

VLFALDETVSES

CDS

/chromosome="I" /clone="T23D8

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FT.	DPDIPSKKIMRTILRTLQEQNPGLIECPLVFDGIHTVYSTELINVKEVNNSVINVAGV
FT 、	NTKESPNLFKLYLTHVDSFLLDTKIITGNQDQNQKLRMMHAIDTVFRQTSTGNFHAVL
FT	SFF S I AQNSA I EP SHGLGAGTVN LGVGREVCYGF YQN VVETFDTLTMN LDVATTFFYR
٦ <u>١</u> ٩	VALVEFLAET LEVP LATVTDGRS LSDVQKKKFNREVAGLKVETRHCSCPRRFRVARCT
FT.	KPTENISFHLSETAGYODSKPLSIVEYYKARYNIDLTYKHLPCIEVGRTRECILPLEL
FT.	YVV SGQRCIKKLMEQQIANLIRATSRNATERQNAVMSLQNRIKMDNDVNAVKFGLKVE
FT ,	QLLKIEGRVLPVPRLLYRSPNIKRQECVTVPNNGTWDMRGKNFYSGIQIREWAIVCFA
FT.	PEI IGEASMRSFVRNLVNVASEIGMPFLEEHRFCRYAEPDQTVKLLEHLNEQYNLQLV
FT	CIVPGKSVVYGELKRKGELLGLTTQCVRSQNVSKASPHTLSNLCMKINSKLGGINVIL
FT	SPPQSINSEPVLF1GCHLTRSSLASSSDSTSSIAHCDSSIACLVGSMDGHPTQFSP1F
7 T.T.	TQPRHQRTIVDMCEMTREAIINFRKSTGFKPHKIIIYRAGIADVTVDEIMQTELRAVR
FT ,	ACAMIEYGFQPGITFIGLDVTHHTRLFAANEKDRVGNSQNVPAGTLVETGITVANLFE
T.	YLVSHAGIQGTSRPTKYVVMMDDNSIPSADIHEMTYQLCHTQSRCTRSVSIPSPVYYA
FT CDS	LVAQRAKILMADENFDMERFRLCVSWF" complement (join (1072310767,1121211658,1170711823, 1247712917,1324913431)) /product="T2208.3"
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F- E-	EST CEESF93FC comes from this
T. E.	/dd xrei= rid:e304440 /tranglation="MGKRKAFIDKKASQSFRLVPDNRERSERFKPTQEHLEEQQKYGV
. T.T.	YDDDYDYLQHMRAVNEPMKLENVHEEVEKTTIKTSGSSAFPPAPPLFGLVGALKKPEF
FT	DEDVANALEEVTDDRNTGELEDNFITLAGGLLDERTTVYRSTRRGEDSEEEEDDDEDD
т. л .	MYDDYNDDELFGEEAVGEIRVERADQRVIDNAFEELMDREYNTDQIGELDGDDYDVGG
FT	LEPNAGRLHKLINDKGPSNAEYDEELAKHYVRERMRLIEEGVIKDKEEYEIVEVDEGT
e: remainder	of annotations omitted.
Query Match	7.1%; Score 52; DB 8; Length 34576;

Query Match
1.1%; Score 34; UB 8; Lengun 343/8;
Best Local Similarity 40.1%; Pred. No. 2.64e-06;
Matches 120; Conservative 44; Mismatches 130; Indels 5; Gaps 5;

AARCAR 258 The start of this sequence (1..10 sequence CET24D1.

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The true left end of clone 123D8 is at 1 in this sequence. The true Direct Submission
Submitted (21-OCT-1996) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 IRQ, England and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jes88anger.ac.uk or rwênematode.wustl.edu overlapping sections once, or longer because we arrange for a small 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. IMPORTANT: This sequence is NOT necessarily the entire insert of clone T23D8. It may be shorter because we only sequence Fulton, L., Gardher, A., Gızen, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P. right end of clone T23D8 is at 34576 in this sequence. The true right end of clone T24D1 is at 12749 in this sequence. Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green, ms in preparation), and other 3087 t-cgaaaaaccaattcaaccatgtcgagaattgtgtttatctgcaaaaaatggatgcgag 3145 259 TGYCAYCCNCAYACNAARAARTTYYTNTGYMSNYTNTTYGCNCCNGTNTGYYTNGAYGAY 318 sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Caulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., 26-NOV-1996 Current sequence finishing criteria for the C. elegans genome available information. The start of this sequence (1..104) overlaps with the end of Secernentea; Rhabditia; Rhabditida; Rhabditidae; Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; ΝI overlap between neighbouring submissions. Caenorhabditis elegans cosmid T23D8 Nature 368 (6466), 32-38 (1994) 94150718 ::: = -:: = ---DNA Caenorhabditis elegans. Caenorhabditis elegans (bases 1 to 34576) 34576 bp (bases 1 to 34576) Caenorhabditis. q1628237 CET23D8 Wild, A. elegans 281128 13 DEFINITION ORGANISM TITLE JOURNAL JOURNAL MEDLINE ACCESSION AUTHORS REFERENCE AUTHORS KEYWORDS REFERENCE COMMENT SOURCE 용 g δ යු ð õ

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Bource FEATURES

CDS

Location/Qualifiers	: .	GIHQILSAYLLAARSFLETTILDLDNHHVQCAAPEFVHCFRQEFEVCQTS"
34576 organism="Caenorhabditis elegans"	CDS	complement (join (1388314240,1429215409,1545616341, 1642316656.1670516807.1766817721.1777418278.
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CKNLDYNQTVFPNLLGHTYQSEAGPATAQENPLIKVKCSEDIRLFLCTVYAPVCTVLE KOTODORI OT SARNGGESI MKKFGENGADINI I DANKFDVTDI CVCKNSERS SNSKKSS		RCYSSNGSTCENVNPEMMOMNITQAAEQAIRLMFNTPDPMQRLHMAKTIRTWIRQDKF AOVDGANMDNCVOOTINTTYDGIKPOPVOLDTSVYAOLMYNILDITRRFTFIPTIFTSPY
RY I OF CREDILINARIA GENERAL OF WIT DO LINGUIS FY INDOVERNING SENSINARIA NDVTFGVSTIANEVVLSPRKCPHHMITTSGSHFSLPLLSGRIPECSLTCEADNQVPMM		INQVOQMECPRENGPQDERELICULISLNWQXDPHMKHCANQVFQIFNCIIMGVKNEK
FDGRVRRILRIMTAAMSVACFVCSLFTLVTFLVDLSRFAYPVRPTLYLAFCYLAISTV		LRTEFAQHLKFEKLVGTLSEYFNPQVHPCMINPAIFIIFRIISKDTRLKDYFIMNN pubopopopotitinnavminevolitacombetioombetautouttopediiciti
YMI GVVGEDGFACGTIGSTFTILVIQGEENVGCSALAVVHIFFFROSSCAMMLVLCLAM FLAANIKWGAESIAALSPYFHAMGWGVPAVLSVTVLVTNSVDGDVFTGICSVGNINPS		FHDZPEPET 1611 IN LANAYMI GSINLILAGANELILEZANELIZOTI IN TENEDELLE HDSDAIDGEVRSDGVGAITTVVQYPNNDLIRAGCKLLLQVSDAKALAKTPLENILPFL
ALVYFFFTPIVVS1ALGAVILVCGIWSMIRIRSYIKLQHADVERNISKLEKIMIRIGA		LRLIEIHPDDEVIYSGTGFLSNVVAHKQHVKDIAIRSNAIFLLHTIISKYPRLDELTD
FAIMYSLPTAMNAAIMMYQAVNMPAMIEGMIHHRCVRLQDREIFGFTYPVDDCPMDPK VAAPEIIVFLLKYVSQLVVGITCAIWVVSSKTLSSYHKAYLALSSRSPTVPAHVDQVN		APKRNRVCEIICNCLATLNNFLMMWIPTPNGETKTAGFNEKQQVCKFIELDILKKLMS CLSCEGMDTPGLLELRSTILRSFILLLRTPFVPKDGVLNVIDENRKENLIGHICAAYS
		WVFRQPINITRTQSTKQQLVERTISLLIVIMEQCGAEKEVAQYSYSIDCPLNLLINGNQV KDFGTUNITIVIVCRITERODTBBJIMTINBBJIECITNHBNSGTAKANSII.SREPEN
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LGDERLATPILLLVIGSLCTLLGFLGCCGAIRENYCLTVSFAVLLALLITGWYRTHES		EDENIKDDTQEYRIQGSILIAVQRLDGELAKILQNADCHSNDYIEKLKAEKDMCSLIE
RGVESAMDKTHQLFECCGVTNSSDWLTFTTLFDSCCLEELEGCARENAPLFEPGCLHS VEOWVIKNGAMVGGTCAVIAATOIVGVCFACCISKSTIKDFHPFYY"		KAŁKY VELKNUSGIEDKHEV CKVIMMRIEHAIIN IQUQNEEDAGKLMUILLOKIIILD DEKRIRORAMICHVYYLAVHDKWHRARDILLIMSHMOAIVDHSDVDTOILYNRTICQLG
complement (join (1072310767,1097811142))		LCAFRHGFIREAHQGLSEIQNTQRAKELLAQAVGTRQHEKTAEQEKIDRSRQVPYHMH
ein predicted using Genefinder"		INVELMECVY LICSMLLETPHMASCEFEMRRMLSRSFHYQLKQSEKASLTGPPENTR FULMAA AKAMI NOPMKKOONY IVANKANOKUMNI FHUA FTUKOMUMBI IOFFSI BTVI.
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		ARIVTKFNVLLGLFNI"
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FFDEDVANALEEVTDDRNTGELEDNFITLAGGLLDERTTVYRSTRRGEDSEEEEDDDE		/codon_start=1
DDEMYDDYNDDELFGERAVGETRVERADQRVIDNAFEELMDREYNTDQIGELDGDDYD 1970a i pain od 1921 tank oddan bordei a gwymedamd i pegytyddrenyddig		/product="T23D8.j" /db vrof="DID:0275022"
V GOALDE PROBLEMANT HONGE OWELD DE LAND I V REGUNDLEEGS TRUNKELEELV V. DEGTINKAKKIDCESFATOYTHI YIHP TLIKEPRGISRKALKREDKAVEEMDIAEEDED		/db_xref="PID:g1628247"
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1385514139	č	FSR"
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Submitted (21-0CT-1996) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: overlapping sections once, or longer because we arrange for a small /translation="MHRHILILELEGCLSADQRLSSTSISSMNGFSTTRKCEHITIPM CKNLDYNQTVFPNLLGHTTQSEAGPAIAQFNPLIKVKCSEDIRLFLCTVYAPVCTVLE KP I QPCRELCLSAKNGCESLAKKFGFQWPDQLDCNKFPVTDLCVGKNSSESSNSKKSS NDVTFGVSTIANEVVLSPKKCPHHMHTTSGSHFSLPLLSGRLPECSLTGEADNQVPMM FDGRVRRILRIWTAAWSVACFVCSLFTLVTFLVDLSRFAYPVRPILYLAFCYLAISTV YMIGVVGEDGFACGTYGSTPTTLVTQGGENVGCSALAVVHYFFFMSSCAWWLVLCLAW FLAANLKWGAES IAALSPYFHAMCWGVPAVLSVTVLVTNSVDGDVFTGICSVGNLNPS alvyffftpivvslalgavllvcgiwsmirirsyiklqhadvernisklekimiriga FA IMYSLPTAMNAA IMWYQAVNMPAWLEGWLHHRCVRLQDRELFGFTYPVDDCPMDPK VAAPEIIVFLLKYVSOLVVGITCAIMVVSSKTLSSYHKAYLALSSRSPTVPAHVDQVN Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnst, M., L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. This sequence is NOT necessarily the entire insert of Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Spreat, J. and Wohldman, P. dye primer and dye terminator reaction, from distinct subclones. overlap between neighbouring submissions.
The true left end of clone T23D8 is at 1 in this sequence. The tright end of clone T23D8 is at 34576 in this sequence. Tho true right end of clone T24D1 is at 12749 in this sequence. Coding using the sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both /note="protein predicted using Genefinder; Similarity Drosophila Tissue polarity protein (TR:024760)" Current sequence finishing criteria for the C. elegans genome The start of this sequence (1..104) overlaps with the end of sequences below are predicted from computer analysis, using program Genefinder (P. Green, ms in preparation), and other complement (join (7258..7391, 7494..7638, 8798..8860, 9211..9343,10019..10101,10150..10212)) join (2786..3258,3758..4122,4187..4325,4866..5107, 5220..5340,5688..5906,6332..6479) clone T23D8. It may be shorter because we only sequence Exceptions are indicated by an explicit note. /organism="Caenorhabditis elegans" jas@sanger.ac.uk or rw@nrm.tode.wustl.edu /db\_xref="PID:e275930" /db\_xref="PID:g1628244" Nature 368 (6466), 32-38 (1994) Nocation/Qualifiers /product="T23D8.1" /chromosome="I" /codon start=] available information. /clone="T23D8" (bases 1 to 34576) 1..34576 Direct Submission sequence CET24D1. I MPORTANT: 94150718 elegans source TITLE JOURNAL REFERENCE AUTHORS JOURNAL MEDLINE CDS FEATURES CDS COMMENT 5 Gaps 5;

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83 SSGSRVSDDLYLHP I EENREPFKLI GKP LPSTTGRFLSLLANHFQI TCNGSI I HQYYI RFDPDI PSKKLNRTI LRTLQEQNPGLI ECP LVFDGI HTVYSTEL INVKEVNNSVINVA /tranglation="MSGRGKGGKCLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGV KRISGLIYEETRGVLKVFLENVIRDAVTYCEHAKRKTVTAMDVVYALKRQGRTLYGFG /db\_xref="PID:q1628249" /translation="MEDQWILISAIYDDIJVEKIKVRSSTSSRSTSINVPSLENEFLSS CD63 antigen like; Drosophila tissue polarity protein like; histone translation="MSGRGKGKAKTGGKAKSRSSRAGLQFPVGRLHRILRKGNYAQR" JCAGAPVYLAAVLEYIAAEVLELAGNAARDNKKTRIAPRHLQLAVRNDEELNKLLAGV Join (26949..27068, 27120..27187, 27232..27606, 27661..28621, 28689..28819, 29049..29748, 30273..30464, 30510..30659) H2A; histone H4; Mouse bright protein like; transporter protein. 3087 t-cgaaaaaccaattcaaccatgtcgagaattgtgtttatctgcaaaaatggatgcgag 3145 2910 ttccaatgtgcaaaaatctggattacaatcaaacagtatttccaaatcttctcggacata 2969 140 TNCARYTNTGYCAYGGNATNGARTAYCARAAYATGMGNYTNCCNAAYYTNYTNGGNCAYG 199 200 ARACNATGAARGARG-TNYTNGARCARGCNGGNGCNTGGATNCCNYTNGTNATGAARCAR 258 3146 tcattaatgaaaaagtttggatttcaatggccagatcaattggattgtaacaaattccc 3204 01-MAR-1997 Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Length 34576; /note="protein predicted using Genefinder" 'note="protein predicted using Genefinder" 44; Mismatches 130; Indels ΝI Rhabditidae; Peloderinae; Caenorhabditis. Pred. No. 2.64e-06; DB 38; Caenorhabditis elegans cosmid T23D8. TIAQGGVLPNIQAVLLPKKTGGDKE' 'db\_xref="PID:g1628248" 'db xref="PID:e276250" /db\_xref="PID:e275933" Score 52; product="T23D8.k" 'product="T23D8.1" SNA Note: remainder of annotations omitted. /codon start=1 Caenorhabditis elegans. /codon start= Caenorhabditis elegans 26277..26660 34576 bp (bases 1 to 34576) 7.1%; Best Local Similarity 40.1%; Conservative q1628237 CET23D8 Wild, A. 120; Query Match Dec 9 09-05 DEFINITION ORGANISM Matches ACCESS 10N AUTHORS REFERENCE S 9 KEYWORDS SOURCE Locus

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protein predicted using Genefinder; Similarity to lat CD63 antigen (SW:P28648) 'db xref="PID:e276248" 'product="T23D8.2"

J.GDERLATPILLLVIGSLCTLLGFLGCCGAIRENYCLTVSFAVLLALLITGMVRYHES RGVESAWDKTHQLFECCGVTNSSDWLTFTTIPDSCCIEEIEGCARENAPLFEPGCIHS /db\_xref="PlD:g1628243" /translation="MVEGGVTIVKYLLFLANLVLWVGGLSLIIVGSILQLKFDNVLDI VEQWVIKNGAMVGGICAVLAAIQLVGVCFACCLSKSILKDFHDFYY" complement (join (10723..10767,11212..11658,11707..11823, 2477..12917,13249..13431))

CDS

/note="protein predicted using Genefinder; cDNA EST cm16f9 comes from this gene; cDNA EST CECSF93R comes from this gene; cDNA EST CECSF93FC comes from this gene"

/codon\_start=1

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complement (join (13883..14240,14292..15409,15456..16341, 16423..16656,16705..16807,17668..17721,17774..18278, 18330..18656,18888..19113,19170..19705,19751..19828, 19884..19991,20041..20214))

CDS

/note="\$imilarity to Yeast nuclear transport protein (SW:P32497); cDNA EST yk44d4.5 comes from this gene; cDNA EST yk33b1.5 comes from this gene; cDNA EST yk33b3.5 comes this gene; cDNA EST yk44d4.3 comes from this gene; cDNA EST yk37b1.3 comes from this gene; cDNA EST yk33bi.3 comes /k8e5.3 comes from this gene; cDNA EST yk8e7.3 comes from from this gene; cDNA EST yk8e5.5 comes from this gene; cDNA EST yk8e7.5 comes from this gene; cDNA EST yk37bl.5 comes from this gene; cDNA EST yk4b7.5 comes from this gene; cDNA EST yk4b7.5 comes from this gene; cDNA EST from this gene; cDNA EST yk37d3.3 comes from this gene"

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AVHDKWHRARDLLLMSHMQAIVDHSDVDTQILYNRTICQLGLCAFRHGFIREAHQGLS EIQNTQRAKELLAQAVGTRQHEKTAEQEKIDRSRQVPYHMHINVELMECVYLICSMLL EIPHMASCEFEMRREMLSRSFHYQLKQSEKASLTGPPENTREHVVAASKAMLNGDWKK CQDYIVNDKMNQKVWNLFHNAETVKGMVVRIQEESLRTYLLTYSTVYATVSLKKLAD LFELSKKDVHSIISKMIIQEELSATLDEPTDCLIMHRVEPSRLQMLALNLSDKLQTLA NAKI SDHMEYETFMTTLQTVNSLLDLLIGTDRVKLSVTYAEEDEN LKDDTQEYR I OGS ILIAVQRLDGELAK ILQNADCHSNDY IEKLKAEKDMCSLIEKAEK YVELRNDSGIFDK HEVCKVYMMR I EHA YYKYODONEEDAGKLMDYLCNK I YTLDDEKR LRQRAMLCHVY Y I ENNEQ I LEPRTGRGGYQGPGSWFPGRNERQGDKQKGSGGYQGERRGGQGQDGKRGNWC

/note="protein predicted using Genefinder; Similarity to complement (25597..25908) SOGGOORRHPOKPRAF"

CDS

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histone H4

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/db\_xref="PID:q1628239" /translation="MSGRGKGGKGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGV KRISGLIYEETRGVLK 7-'LENVIRPAVTY CEHAKRKTVTAMDVVY ALKRQGRTLYGFG

26277..26660

CDS

/note="protein predicted using Genefinder; Similarity to histone H2A; cDNA EST yk72a2.3 comes from this gene; cDNA EST yk124d7.3 comes from this gene; cDNA EST yk124d7.5 comes from this gene; cDNA EST yk72a2.5 comes from this

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/db\_xref="PID:g1628248" 'db\_xref="PID:e276250"

/translation="MSGRCKGGKAKTGCKAKSRSSRAGIQFPVGRLHRILRKGNYAQR VGAGAPVYLAAVLEYLAAEVLELAGNAARDNKKTRIAPRHLQLAVRNDEELNKLLAGV TIAQGGVLPNIQAVLLPKKTGGDKE"

join(26949..27068,27120..27187,27232..27606,27661..28621, /note="protein predicted using Genefinder; cDNA EST yk116f3.3 comes from this gene; cDNA EST yk20f1.5 comes 28689..28819,29049..29748,30273..30464,30510..30659)

CDS

from this gene; cDNA EST yk116f3.5 comes from this gene" /product="T23D8.7" /codon\_start=1

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Note: remainder of annotations omitted.

7.1%; Score 52; DB 111; Length 34576; Query Match

Best Local Similarity 40.1%; Pred. No. 2.64e-06;

5; 2910 ttccaatgtgcaaaaatctggattacaatcaaacagtatttccaaatcttctcggacata 2969 3029 igctcagaagataticgictititititigiacigictaigcaccigicigiacag-i-ac 3086 3087 t-cgaaaaaccaattcaaccatgtcgagaattgtgtttatctgcaaaaaatggatgcgag 3145 140 INCARYTHTGYCAYGGNATNGARTAYCARAAYATGMGNYTNCCNAAYYTNYTNGGNCAYG 199 1 (bases 1 to 215)
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use to 200 ARACNATGAARGARG-TNYTNGARCAF.GCNGGNGCNTGGAINCCNYTNGTNATGAARCAR 258 71 nnvgaakthyythtnvsgadsktvtdsynasgtsssnggtdgnrsgadsygssktamtsr 130 233 GCNCCNG-CYTGYTCNARNACYTCYTTCATNGTYTCRTGNCCNARNARRITNGGNARNCK 175 131 nrtgktannavdsrnmgdasvgsdkntkkhaknsadgk-vgsknngdrnnrygtgtksnv 189 30-0CT-1996 Gaps Gaps 5; 5; Score 49; DB 57; Length 215; Pred. No. 4.18e-05; 81; Mismatches 98; Indels 141 others Indels PAT 44; Mismatches 130; 26 t control fungal disease
Patent: US 5569830-A 5 29-0CT-1996; 128278 215 bp DNA Sequence 5 from patent US 5569830. 128278 /organism="unknown" 190 snncgggnkrdvssyannkccgssct 215 Location/Qualifiers 25 g ::|:::| 114 NWSNCKYTTRTANWSRAARTCNGGYT 89 Query Match 6.7%; Best Local Similarity 12.1%; Matches 25; Conservative ပ ထ Conservative 1..215 Unclassified. 15 a g1819054 Unknown. Unknown. Matches 120; DEFINITION RESULT 15 source ORGANISM BASE COUNT ORIGIN REFERENCE AUTHORS ACCESS ION JOURNAL KEYWORDS FEATURES TITLE SOURCE LOCUS QIN අ අු 유 ð g ð ð ð ð 음 g. 엄 გ g გ g

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch nn

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Tue Dec 9,10:11:03 1997; MasPar time 92.45 Seconds 931.301 Million cell updates/sec •

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>848439-3-trans

(1-825) from translate.seq Description: Perfect Score:

1 WSNGCNMGNGGNYTUTTYT.......SNATNMGNAARYTNCARTGY 825 SWNCGNKCNCCNRANAARRA.........wntankcnttyrangtyacr N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 •• STD Nmatch 142080 seqs, 52183452 bases x 2 Searched:

Listing first 45 summaries Minimum Match 0% Post-processing:

Database:

iparti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part21 28:part28 n-geneseq28

Mean 11.254; Variance 12.824; scale 0.878 Statistics: ,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query core Match Length DB ID	DB	e e	Description	Pred. No.
-	1 122 17.7 1047 2 010572	17.7	1047	2	Q10572	Human Natriuretic Pep	3.70e-29
2	66	14.4	1047	7	010572	Human Natriuretic Pep	3.46e - 21
c / 3	53	7.7	501	က	N50030	Sequence encoding new	5.08e-06
c / 4	23	7.7	501	ო	N50027	Sequence encoding new	5.08e-06
5	53	7.7	565	9	935072	HCV envelope region n	5.08e-06
9	52	7.6	501	n	N50033	Sequence encoding new	1.04e-05

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encoding			-		Sequence encoding new				Sequence encoding new	·	Sequence encoding new		Sequence encoding new	Sequence encoding new	St quence encoding new		Sequence encoding new	Sequence encoding new	Sequence encoding new	HCV ervelope region n		ase substituted	Base substituted E.co		Oligonucleotide probe	ы	Sequence encoding new		Φ			a		V.fischeri flavin red	Degenerate Alteromona	[Iz	V.fischeri flavin red	Sequence encoding Pla
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498	501	501	501	501	501	501	501	501	501	984	501	498	501	501	501	501	501	501	501		501	204	204	657	91	91	501	114	984	1065	3871	3871	657	711	1065	420	711	166
7.4	7.4	7.4	7.3		7.3	7.1	7.1	7.1	7.1	7.1	•		8.9	8.9	٠.				6.5		6.2			0.9		5.7		5.7			5.7		5.5	5.4	5.4		4.9	
51							49	49	49	49	48	47	17	ij	47	47	45	45	45	45	43	42	41	41	40	39	39	39	39	39	39	39	38	37	37	32	34	33
7	œ	6	10	11	12	13	14	15	16	17	18	19	70	21	22	23	24	52	56	27	88	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
PPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase; hyperaldosternnism; glaucoma; guanyl cyclase. /label= extracellular domain /note= "binds natriuretic peptides A,B and C]" Domain 456..456 Location/Qualifiers LT 1 210572 standard; DNA; 1047 BP. Q10572; /label= transmembrane domain Domain 479..1047 23..455 /label= signal sequence 1..22/label= mature NPBR Homo sapiens. Peptide Protein Domain Domain 

/label= cytoplasmic domain /note= "GC and protien kinase activity"

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E	Modified -site 2426	δλ	
	/labei= N-glycos site Modified -site 35.37	qq	
댎	/label= N-glycos_site Modified -site, 161,163 **;^	Qy	
댎		qq	
FT	/label= N-qlycos site Modified -site 744246	δλ	
FT	/label= N-glycos site Modified -site 277279	QQ	
FT	/label= N-glycos site Modified -site 349351	'n	
담담	/label= N-glycos site Modified -site 600602	අු	
FT		δ	
PD PF	10-JAN-1991. 22-JUN-1990; U03586.	qq	
PR PA	23-JUN-1989; US-370673. (GETH ) GENENTECH INC.	δλ	
PI DR	Chang M, Goeddel D, Lowe D; WPI; 91-036711/05.	qq	
P. T.	N-PSDB; Q10324. Natriuretic protein receptor B - for diagnosis and treatment of	6y	
PT PS	kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.	qo	
ខ្ល	The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having quanyl cyclase (GC) activity and protein	ò	
ខ្លួ	kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce	୍ ପ	
ខ	NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=	ė	
ខខខ	114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptided using affinity chromatography. Antibodies with affinity for NPRB can	δŏ	
ខម	also be prepd.	RESULT	ΗC
3	104/ BF; 8/ A; 15 C; 83 G;		S CO
2 8	Ouery Match 17.7%; Score 122; DB 2; Length 1047; Best Local Similarity 12.3%; Pred. No. 3.70e-29;	ם	0 X
Wa			Z .
a :	177 drnhyntnngvnnanngennsvnhnvyarnnggnnnathnnrangrnvyncgnnnmnhnn 236   :: ::           :: :    :: : : : :     CCNVTNNTVVNNTTVCCNCTAPTOCKNTAVEKNTAVARNATAVEKNAAVEKAAATION	S F.F.	1 H X 0
<u> </u>			- 6
g &	237 nnnanrnnntngdyvnnyndvngnsnragntratgrnwndnrtrnnananrnanntvnvn 296     : : : : : : : : : : : : : : : : : :		- A
ନୁ	297 tyrnnnnnnynnnnnrarnnnrarndngvnngnsnmnnnagcnydgnnnyanvnnntnnngg 356	FF	~~ ¢
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ò	:  : : : :  :  :  :    :       :   :		~ Z \
qq	417 nnwwtgrnnnwykgannsdnnncandnddnscdktnnstnanvangtgntnnmngvssnn 476		× Z \
δy	248 CYYTINGAYGAYTINGAYGARACHATINCARCCHTGYCAYMSNYTINTGYGTINCARGTINAARG 307		Σ.
g	477 nnrknmnknnasmnw-rnrwnnnnngnenryhkgagsrntnenrgesygsnmtahgkyn 535 ::  :       : : : :       : : : :	FT	Σ \

δ	308 AIMGNIGIGENCENCINATEMSNGENITIGGNITICENTEGEENGAIATGIINGAKTGIG 35/
QQ	536 nnantghnkgnvvankhvnkkrnnntrnvnnnnkhmrdvnnnhntrnngaendnnnenv 595
0y	368 AYMGN-TTYCCNCARGAYAAYGAYYTNTGYATNCCNYTNGCNFNSNGAYGAYTNYTN 426
QQ	596 tnycnrgsnndnnndsnnndwmnrysnnndnvkgmannhnsnnsshgsnkssncvvdsr 655
δy	427 CCNGCNACNGARGARGANCCHAARGTNTGYG-ARGCNTGYAARAAYAARAAYGAYGA 485
qq	656 nvnkntdygnasnrstannddnnanyakknntannnnsgnnnttgmnaadvysngnnnn 715
δ	486 YAAYG-AYATNATGGARACNYTNTGYAARAAYGAYTTYGCNYTNAARATNAARGTNAARG 544
qq	716 nnanrsgnnynngndnsnknnvnkvrngnrnynrnsndrtnnnnnvnnmnrcwandnan 775
ζ	545 ARATNACNTAYATNAAYMGNGAYACNAARATNATNYTNGARACNAARWSNAARACNATNT 604
qq	776 rndngnnkgnnrrnnknggtsnndnnnrmnnyannnnknvnnrtnaynnnkrkananny 835
Qγ	605 AYAARYTINAAYGGNGTUHISNGARMGNGAYTINAARAARHSNGTUYTINTGGYTIN-AARGAY 663
d d	836 nnnnhsvannnkrgntvnanandsvtnynsdnvgntansanstnmnvvtnnndnytcnda 895
δ	664 WSNYTWCARTGYARUTGYGARGARATGAYGAYATNAAYGCNCCNTAYYTNGTNATGGGN 723
eg G	5
δλ	724 CARAARCARGGN-GGNGARYINGINAINACNWSNGTNAARMGNIGGCARAARGGNCARMG 782
qq	ıgvhtgı
φ	
RESULT	2 271
8	Q10572 standard; DNA; 1047 BP.
AC	010572;
E B	09-Ark-1991 (lirat entry) Human Natriuretic Peptide Receptor B.
<b>X</b>	NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
S S	nyperaldosteronism; glaucoma; guanyi cyclase. Homo sapiens.
F	
Ŀ	Peptide 122 /label= simal_segmence
E	Protein 12
i i	/label= mature NPBR Domain : 23455
E	= extracellular domain
FT	/note= "binds hatriuretic peptides A, B and C]"
I I	/label= transmembrane domain
FT	Domain 4791047
LE	/label= cytopiasmic domain /no:e= "3C and protien kinase activity"
FT	Modified -site 24.26
F	/label= N-glycos site Modified -site 3537
FT	/label= N-glycos site
F	Modified -site joi
FT	Modified -site: 195.197
FI	/label= N-glycos_site

Modified -site

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N-PSDB; Q10324.

WO9100292-P 10-JAN-1991 also be prepd

Sequence Query Match

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2; 143 10 ytbaayggnmgdytbgartaytgyytbaargaymgdcaygayttymgdathccncargar 129 130 garttygayggnaaycarttycaraargargaygcngcnytbacnathtaygaratgytb 189 190 caraayathttygcnathttymgdcargaywnnwnnwnnacnggntggaaygaracnath 249 460 CYTCRCANACYTTNGGNGCYTCYTCNGTNGCNGGNARNARRTGRTCNWSNWSNGCNARNG 401 262 CNARRICRICNARRCANACNGGNGCRAANARNWSRCANARRAAYTTYTINGIRICNGGRT 203 83 10 aayytbytbggnttyytbcarmgdwnnwnnaayttycartgycaraarytbytbtggcar 69 INFs of the invention are more active and have different affinities have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 50; Bp; 110 A; 31 C; 69 G; 79 T; 3; Gaps 911 aymvvsgnngrngnrhannnarmananndavssnrnrhrnhdnnrnrngvhtgnvcagvv 04-SEP-1991 (first entry) Sequence encoding new modified human beta interferon polypeptides IENX 447. 852 vnanandsvtnynsdnvgntansanstnmnv-vtnnndnytcndanndnndvykvntngd 202 GRCAYTGYTTCATNACNARNGGNATCCANGCNCCNGCYTGYTCNARNACYTCYTTCATNG 142 TYTCRTGNCCNARNARRTTNGGNARNCKCATRTYTGRTAYTCNATNCCRTGRCANARYT 400 GNATRCANARRICRTIR--ICYTGNGGRAANCKRICRCAYICN-ARCAIRICNGGCCANG Compared with interferon beta prepd. by recombinant methods, the for cell surface receptors (allowing selective targetting); they 971 gnkmnrycnngdtvntasrmnsngnanknhvssttkdandnngcnnnnnrgdv 1023 ል New modified human beta interferon polypeptide(s) - prepd. Antiviral; cell growth regulator; immune system regulator, DB 3; Length 501; 39; Conservative 187; Mismatches 260; Indels plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions Claim 28; Chart 2h, page 39; 71pp; English. Pred. No. 5.08e-06; 7.7%; Score 53; Location/Qualifiers 17-WAY-1985, 105750. 17-WAY-1984; GB-012564. (SEAR ) SEARLEG D & CO. Bell LD, Boseley PG, Porter AG; WPI; 85-311944/50. N50030 standard; DNA; 501 BP Query Match 7.7%; Best Local Similarity 8.0%; antiproliferative; ss. P-PSDB; P50029. = Homo sapiens /\*tag= a EP-163993-A. 11-DEC-1985 Matches გ 셤 셤 გ g ც 셤 c 셤 გ g g, g 432 nnsdnnncandnddnscdktnnstnanvangtgntnnmngvssnnnnrknmnnknnasmn 491 621 NACNCCRTTNARYTTRIANATNGTYTTNWSYTTNGTYTCNARNATNATYTTNGTRICNCK 562 492 wrnrwnnnnngnanryhkgagarntnanrgsayganmtahgkynnnantghnkgnvvank 551 RTTNATRIANGTNATYTCYTTNACYTTNATYTTN-ARNGCRAARTCRTTYTTRCANARNG 503 hvnkkrnnntrnvnnnnkhmrdvnnnhrtrnngacndnnncnvtnycnrgsnndnnnd 611 502 TYTCCAINAIRICRITRICRICRITYIIRITYTIRCANGCYICRCANACYTINGGNG 443 ennndwmnryennndnvkgmannhnsnneshgenkeencvvdsrnvnkntdygnasnret 671 CYTCYTCNGTNGCNGGNARNARRIGRICOWSNWSNGCNARNGGNATRCANARRICRITRT 383 382 CYTCNGGRAANCKRICRCAYICNARCAIRICNGGCCANGGRAANCCRAANGCNWSCAINA 323 791 322 CNGGNGCRCANCKRTCYTTNACYTGNACRCANARNWSRTGRCANGGYTGNATNGTYTCRT 263 nggtenndnnnnrmnnyannnnknvnnrtnaynnnkrkanannynnnnhsvannnkrgnt 851 681 RCANGTRCAYTGNARNWSRTCYTTNARCCANARNACNWSYTTYTTNARRTCNCKYTCNWS 622 annddnnanyakknntannnnsgnnnnttgmnaadvysngnnnnnnanrsgnnynngndn 731 372 ryhgytgnyvmdknndrntdnynwamgdndsgdnnnaahysganknnwwtgrnnnwykga 431 The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having quanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analoques. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of Gaps 732 snknnvnkvrngnrnynrnsndrtnnnnnnvnnmnrcwandnanrndngnnkgnnrrnnk natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. 2; 14.4%; Score 99; DB 2; Length 1047; 12.4%; Pred. No. 3.46e-21; 81; Conservative 178; Mismatches 392; Indels 51 T; .. -83 G; 15 C; ----Claim 3; Fig 1; 49pp; English. 87 A; Chang M, Goeddel D, Lowe D; WPI; 91-036711/05. /label= N-glycos site Modified -site 600..602 /label= N-glycos\_site Modified -site 277..279 /label= N-glycos site Modified -site 349..351 23-JUN-1989; US-370673. (GETH ) GENENTECH INC. /label= N-glycos site 22-JUN-1990; U03586. Best Local Similarity Matches 81; Conserv :: <u>:-</u> -1047 BP;

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Db 113 tygqnathcongargarathaarcarytbcarcarttycataargargaygcngcnybb 172	Cp 428 GGNARNARTGRTGNWSNWSNGCNARNGGNARRTCRTTRTCYTGNGGRAANCKR 369  Db 350 tgwnnwnnytboayytbaarmgmtaytayggnmgdathytbcaytayytbaargcnaarg 409    1	Ins	PT virus (1), for producting vaccine PS Claim 1; Page 2; 13pp; Japanese. CC This sequence encodes a novel envelope region of type C hepatitis CC Virus (HCV). This fragment can be used for the preparation of a CC vaccine for hepatitis C. This fragment was prepared from the serum CC vaccine for hepatitis C. This fragment was prepared from the serum CC of non-A, non-B hepatitis patients and the envelope region DNA was CC amplified by PCR using the primer sequences given in Q35073-76. SQ Sequence 555 BP; 61 A; 92 C; 106 G; 85 T; Query Jat.;h Rest Local Similarity 13.7%; Score 53; DB 6; Length 565; Rest Local Similarity 13.7%; Preca. No. 5.08e-06; Matches 61: Conservative 160: Mismatches 718: Indels 5; Gans 5;	yytdccygttgcycttytctatcttyctyytrgcyytbctytcytgyytgacyrybcc 119 ::   :   :   : : :         : : : : :   :   :   :         :
	Cp 163 GYTCNARNACYTCTTCATNCTYTCRTGNCCNARNARRTTNGGNARNCKCATRTYTGRT 104  Db 430 acnathgtnmgdgtngarathytbmgdaayttytaytthaaymgdytbacnggntay 489	nbe	PT New modified human beta interferon polypeptide (8) - prepd. by PT plasmid transformed bacteria, with improved antiviral, T anti-proliferative and immune regulating actions PS claim 28; Chart 2e, page 36; 71pp; Endlish. CC Compared with interferon beta prepd. by recombinant methods, the CC INFS of the invention are more active and have different affinities CC for cell surface receptors (allowing selective trageting); they have higher therapeutic index; improved stability against microbial CC breakdown during synthesis; and better in vivo solubility and CC stability. They are also easier to recover from incubation mixts. SQ Sequence 501 BP; 112 A; 31 C; 67 G; 80 T;	Ouery Match 7.7%; Score 53; DB 3; Length 501; Best Local Similarity 16.0%; Pred. No. 5.08e-06; Matches 72; Conservative 135; Mismatches.240; Indels 4; Gaps 3; Db 53 araarytbytbtggcarytbaayggnmgdytbgartaytgyytbaargaymgdatgaayt 112

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                                                                                                                                                ccytgygtycgsgarrryrnynnytcbmgntgytgggyrgcgctbacycccacgstygcy 297
                                                                                                                                                                                                                                181 CCNYINGINAIGAARCARICYCAY-CCNGAYACNAARAARITYYTNIGYWSNYINIIYGC 239
                                                                                                                                                                                                                                                                                                        298 rcyagrrayvbyavyvtycccrcbrygvmrmtwcgbcgbcayrtcgayytgctygthggg 357
                                                                                                                                                                                                                                                                                                                                                    240 NCCNGTNTGYTNG-AYGAYYTNGAYGARACNATNCARCCNTGYCAYNSNTNTGYGTNC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 ravgcyrcyytctgytcagcyvtataygtkggrgayytbtgcggrtcygtyttyctyrty 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 ARGINAARGAYMGNIGYGCNCCNGINAIGWSNGCNIIYGGNIIYCCNIIGGCCNGAYAIGY 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CCNAAYYTNYTNGGNCAYGARACNATGAARGARGTNYTNGARCARGCNGGNGCNTGGATN 180
179 cyaackcragyatwgtgyayrarg-yrrmggayryyatcmtgcwydyyccbgggtgyryb 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFs of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 111 A; 31 C; 68 G; 80 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoding new modified human beta interferon polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 28; Chart 2k, page 42; 71pp; English.
Compared with interferon beta prepd. by recombinant methods, the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antiviral; cell growth regulator; immune system regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72; Conservative 135; Mismatches 240; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.6%; Score 52; DB 3; Length 501; Best Local Similarity 16.0%; Pred. No. 1.04e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid transformed bacteria, with improved antiviral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-proliferative and immune regulating actions
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Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N50033 standard; DNA; 501 BP.
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EP-163993-A.
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Claim 28; Chart 21, page 43; 71pp, English. Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities

New modified human beta interferon polypeptide(s) - prepd. by

P-PSDB; P50033

plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions

for cell surface receptors (allowing selective targetting); they

have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence  $498~\mathrm{Bp};~112~\mathrm{A};~30~\mathrm{C};~68~\mathrm{G};~77~\mathrm{T};$ 

7.4%; Score 51; DB 3; Length 498;

Query Match

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173 cnathtaygaratgytbcaraayathttygcnathttymgdcargaywnnwnnacng 232 548 ATYTCYTINACYTINATYTINARNGCRAARTCRTYTTRCANARNGTYTCCATNATRICR 489 tgwnnwnnytbcayytbaarmgdtaytayggnmgdathytbcaytayytbaargcnaarg 409 410 artaywnncaytgygcntggacnathgtnmgdgtngarathytbmgdaayttytayttya 469 308 TCYTTNACYTGNACRCANARNWSRTGRCANGGYTGNATNGTYTCRTCNARRTCRTCNARR 249 488 TTRTCRTCRTCRTTYTTRTTYTTRCANGCYTCRCANACYTTNGGNGCYTCYTCNGTNGCN 429 668 ARNWSRTCYTTNARCCANARNACNWSYTTYTTNARRTCNCKYTCNWSNACNCCRTTNARY 609 368 TCRCAYTCNARCATRTCNGGCCANGGRAANCCRAANGCNWSCATNACNGGNGCRCANCKR 113 tygarttyccncargargarttygaygayaarcarttycaraargargaygcngcnytba 608 TIRTANAINGTYTINWSYTINGTYTCNARNAINATYTINGTRICNCKRITNAIRIANGTN 233 gntggaaygaracnathgtngaraay.tbytbgcnaaygtntaycaycarathaaycayy tbaaracngtn--ytbgargar-aarytbgataargargayttyacnmgdggnaarytba Sequence encoding new modified human beta interferon polypeptides Antiviral; cell growth regulator; immune system regulator; 848439-3-trans.mg <u>::</u> :: 470 thaaymgdytbacnggntay-ytbmgdaayt 499 248 CANACNGGNGCRAANARNWSRCANARRAAYT 218 Location/Qualifiers 11-DEC-1985. 17-MAY-1985; 105750. 17-MAY-1984; GB-012564. (SEAR ) SEARLE G D & CO. Bell LD, Boseley PG, Porter AG; WPI; 85-311944/50. N50034 standard; DNA; 498 BP. 04-SEP-1991 (first entry) antiproliferative; ss. 1..498 Homo sapiens. EP-163993-A. /\*tag= a ENX 485 Dec 9 10:15 N50034; 293 320 g g 셤 გ. 요 გ 임 გ 임 გ a G S a გ.

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g 8888888 임 ð 셤 ð 셤 염 ð g ð ð ð 5 70 ytbaayggnmgdytbgartaytgyytbaargaymgdgcngayt-tyaarathccnatgga 128 GNATRCANARRICRITRICYTGNGGRAANGKRICRCAYTCN-ARCATRICNGGCCANGGR 342 raayathttygcnathttymgdcargaywnnwnnwnnacnggntggaaygaracnathgt 248 520 ARTCRITYTIRCANARNGTYICCAINAIRICRITRICRICRICRITYIIRITYIIRCANG 461 460 CYTCRCANACYTINGGNGCYTCYTCNGTNGCNGGNARNARRIGRICNWSNWSNGCNARNG 401 129 ratgacngaraargarttycaraargargaygcngcnytbacnathtaygaratgytbca 188 341 AANCCRAANGCNWSCATNACNGGNGCRCANCKRTCYTTNACYTGNACRCANARNWSRTGR 282 ngaraayytbytbgcnaaygtntaycaycarathaaycayytbaaracngtnytbgarga 308 CANGGYTGNATNGTYTCRTCNARRTCRTCNARRCANACNGGNGCRAANARNASRCANARR 222 raarytbgaraargargayttyacnmgdggnaarytbatgwnnwnnytbcayytbaarmg 368 AAYTTYTTNGTRTCNGGRTGRCAYTGYTTCATNACNARNGGNATCCANGCNCCNGCYTGY 162 369 dtaytayggnmgdathytbcaytayytbaargcnaargartaywnncaytgygcntggac 428 161 TCNARNACYTCYTTCATNGTYTCRTGNCCNARNARRTTNGGNARNCKCATRTTYTGRTAY 102 nathgtnmgdgtngarathytbmgdaayttytayttyathaaymgdytbacnggntayyt 488 101 TCNATNCCRTGRCANARYTGNARRTTNGCNGGNATNGCYTTRCARTTNWSNCKYTTRTAN 42 10 aayytbytbggnttyytbcarmgdwnnwnnaayttycarwnncaraarytbytbtggcar 69 Gaps Sequence encoding new modified human beta interferon polypeptides 5; ል New modified human beta interferon polypeptide(s) - prepd. plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions Antiviral; cell growth regulator; immune system regulator; Indels ' 39; Conservative 181; Mismatches 265; Pred. No. 2:11e-05; į Claim 28; Chart 2a, page 32; 71pp; English. Location/Qualifiers 1..501 ------(SEAR.) SEARLE G D & CO. ... Bell LD, Boseley PG, Porter AG; WPI; 85-311944/50. N50023 standard; DNA; 501 BP. 8.08; 04-SEP-1991 (first entry) 17-MAY-1984; GB-012564. antiproliferative; ss. 17-MAY-1985; 105750. Best Local Similarity 489 bmgdaay 495 P-PSDB; P50022. 41 WSRAART 35 Homo sapiens. /\*tag= a EP-163993-A. 11-DEC-1985 N50023; Matches 400 189 429 309 221 RESULT

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ï 284 ARATNAARGTNAARGARATNACNTAYATNAAYMGNGAYACNAARATNATNYTNGARACNA 589 166 gcnytbacnathtaygaratgytbcaraayathttygcnathttymgdcargaywnnwnn 225 345 rytbatgwnnwnnytbcayytbaarmgdtaytayggnmgdathytbcaytayytbaargc 404 405 naargattaywnncaytgygcntggacnathgtnmgdgtngarathytbmgdaayttyta 464 Gaps Claim 28; Chart 2f, page 37; 71pp; English. Compared with interferon beta prepd. by recombinant methods, tho INFs of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities have higher therapeutic index; improved stability against microbial stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 107 A; 31 C; 69 G; 80 T; haaycayytbaaracngtnytbgargataarytbgaraargargayttyacnmgdggnaa 226 wnnacnggntggaaygaracnathgtngaraayytbytbgcnaaygtn-taycaycarat Sequence encoding new modified human beta interferon polypeptides Compared with interferon beta prepd. by recombinant methods, the for cell surface receptors (allowing selective targetting); they ;; breakdown during synthesis; and better in vivo solubility and δ New modified human beta interferon polypeptide(s) - prepd. Antiviral; cell growth regulator; immune system regulator; antiproliferative; ss. 95; Mismatches 167; Indels Score 51; DB 3; Length 501; Pred. No. 2.11e-05; plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions <del>::</del> :: :: Location/Qualifiers Bell LD, Boseley PG, Porter AG; WPI; 85-311944/50. N50028 standard; DNA; 501 BP. 7.48; Best Local Similarity 16.0%; 50; Conservative 04-SEP-1991 (first entry) (SEAR ) SEARLE G D & CO 17-MAY:1985; 105750. 17-MAY-1984; GB-012564. 465 yttyathaaymgd 477 110 AYYINGINAIGGG 722 Homo sapiens. P-PSDB; P50027 /\*tag= a EP-163993-A. 11-DEC-1985. Query Match IENX 445. N50028; Matches 285 530 

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have higher therapeutic index; improved stability against microbial
                                                                             They are also easier to recover from incubation mixts.
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                            breakdown during synthesis; and better in vivo solubility and
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                                                                                                                                                                                                                                                         44; Conservative 159; Mismatches 252; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antiviral; cell growth regulator; immune system regulator;
                                                                                                                                                                               / Match 7.4%; Score 51; DB 3; Length 501; Local Similarity 9.6%; Pred. No. 2.11e-05;
                                                                                                             68 G;
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(SEAR ) SEARLE G D & CO.
Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50.
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EP-163993-A.
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Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability: They are also easier to recover from incubation mixts. Sequence 501 BP; 110 A; 37 C; 69 G; 80 T; 233 gntggaaygaracnathgtngaraayytbytbgcnaaygtntaycaycarathaaycayy 293 tbaaracngtnytbgargara--arytbgaraa-rgargayttyacnmgddgnaarytba 368 TURCAYTCHARCATRICHGGCCANGGRANGCRAANGCNWSCATHACHGGNGCRCANCKR Sequence encoding new modified human beta interferon polypeptides 4; 69; Conservative 136; Mismatches 242; Indels Antiviral; cell growth regulator; immune system regulator; Query Match 7.3%; Score 50; DB 3; Length 501; Best Local Similarity 15.3%; Pred. No. 4.27e-05; 470 thaaymgdytbacnggntay-ytbmgdaayt 499 248 CANACNGGNGCRAANARNWSRCANARRAAYT 218 Location/Qualifiers LT 11 N50023 standard; DNA; 501 BP. 04-SEP-1991 (first entry) antiproliferative; ss. Homo sapiens 113 Matches Key 쇰 S 셤 g g გ 셤 გ 숌 გ පු g, g g, 쇰

17-MAY-1984; GB-012564. (SEAR ) SEARLE G D & CO.

11-DEC-1985. 17-MAY-1985; 105750.

/\*tag= a EP-163993-A.

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Query Match

48 Matches

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113 tyggnathccngargarathaarcarggncarcarttycaraargargaygcngcnytba 172
  233 gntggaaygaracnathgtngaraayytbytbgcnaaygtntaycaycarathaaycayy 292
  488 ITRICRICRICRITYITRITYITRCANGCYICRCANACYITNGGNGCYICYICNGINGCN 429
  293 tbaaracngtnytbgargara--arytbgaraa-rgargayttyacnmgdggnaarytba 349
  350 tgwnnwnnytbcayytbaarmgdtaytayggnmgdathytbcaytayytbaargcnaarg 409
   410 artatwnncaytgygcntggacnathgtnmgdgtngarathytbmgdaayttytayttya 469
   53 araarytbytbtggcarytbaayggnmgdytbgartaytgyytbaargaymgdatgaayt 112
  548 ATYTCYTINACYTINATYTINARNGCRAARTCRTTYTTRCANARNGTYTCCATNATRICR 489
   428 GGNARNARRIGRICHWSNWSNGCNARNGGNATRCANARRICRITRICYIGNGGRAANCKR 369
   308 TCYTTNACYTGNACRCANARNWSRTGRCANGGYTGNATNGTYTCRTCNARRTCRTCNARR 249
  INFs of the invention are more active and have different affinities
  have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and
   173 cnathtaygaratgytbcaraayathttygcnathttymgdcargaywnnwnnwnnacng
   | : : :||: |: : :| | 368 TCRCAYTCNARCATRICNGCCRAANCCRAANGCNWSCATNACNGCNGCRCANCKR
  stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 112 A; 31 C_j 69 G_j 79 T_j
   608 TIRIANAINGIYIINWSYIINGIYICNARNAINAIYIINGIRICNCKRIINAIRIANGIN
  Sequence encoding new modified human beta interferon polypeptides IFNX 417.
   for cell surface receptors (allowing selective targetting); they
   Compared with interferon beta prepd. by recombinant methods, the
   New modified human beta interferon polypeptide(s) - prepd.
   Antiviral; cell growth regulator; immune system regulator;
   DB 3; Length 501;
  Conservative 133; Mismatches 242; Indels
   plasmid transformed bacteria, with improved antiviral,
   anti-proliferative and immune regulating actions Claim 28; Chart 29, page 38; 71pp; English.
  Pred. No. 4.27e-05;
   248 CANACNGCNGCRAANARWESRCANARRAAYT 218
   470 thaaymgdytbacnggntay-ytbmgdaayt 499
  31 C;
   7.3%; Score 50;
   Bell LD, Boseley PG, Porter AG; WPI; 85-311944/50.
   112 A;
   ВP
   Query Match 7.3%;
Best Local Similarity 16.0%;
Matches 72; Conservative
   ::
   LT 13
N50024 standard; DNA; 501
  04-SEP-1991 (first entry)
  (SEAR ) SEARLE G D & CO
   17-MAY-1985; 105750.
17-MAY-1984; GB-012564.
  501 BP;
   P-PSDB; P50028
EP-163993-A
   Sequence
   N50024;
   RESULT
ID N5
AC N5
DT 04
DE S¢
DE IE
  염
   გ
   셤
   გ
  음
   ე,
  유
   S,
   셤
  g
   ద
   გ
   원
  g
   원
   g
   ä
  ygayttyggnttyccncargargarttygayggnaaycarttycaraargargaygcngc 167
  nacnggntggaaygaracnathgtngaraayytbytbgcnaaygtntaycaycarathaa 287
   493 IRTCRTTRTCRTCRTCRTTYTTRTTYTTRCANGCYTCRCANACYTTNGGNGCYTCYTCNG 434
   344
   naargattaywnncaytgygcntggacnathgtnmgdgtngarathytbmgdaayttyta 464
  613 TNARYTTRTANATNGTYTTNWSYTTNGTYTCNARNATNATYTTNGTRTCNCKRTTNATRT 554
   168 nytbacnathtaygaratgytbcaraayathttygcnathttymgdcargaywnnwnnwn 227
   433 INCCNGGNARNARRIGRICNWSNWSNGCNARNGGNAIRCANARRICRIIRICYIGNGGRA 374
   345 rytbatgwnnwnnytbcayytbaarmgdtaytayggnmgdathytbcaytayytbaargc 404
  373 ANCKRICRCAYICNARCAIRICNGGCCANGGRAANCCRAANGCNWSCAINACNGGNGCRC 314
   rwnncaraarytbytbtggcarytbmmyggnmgdytbgartaytgyytbaargaymgdca 107
   313 ANCKRICYTINACYIGNACRCANARNWSRIGRCANGGYIGNAINGIYICRICNARRICRI 254
   Gaps
  New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions claim 28, Chart 2a, page 32; 71pp; English Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities
   have higher therapeutic index; improved stability against microbial
  breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 107 A; 31 C; 69 G; 80 T;
   288 ycayytbaaracngtnytbgargata--arytbgaraa-rgargayttyacnmgdggnaa
   Sequence encoding new modified human beta interferon polypeptides
   for cell surface receptors (allowing selective targetting); they
   4;
  <u>::</u>
::
::
   Antiviral; cell growth regulator; immune system regulator;
   7.3%; Score 50; DB 3; Length 501;
   68; Conservative 138; Mismatches 246; Indels
   Pred. No. 4.27e-05;
   465 yttyathaaymgdytbacnggntay-ytbmgdaayt 499
  253 CNARRCANACNGGNGCRAANARNWSRCANARRAAYT 218
  Location/Qualifiers
Boseley PG, Porter AG;
   N50029 standard; DNA; 501 BP
   Best Local Similarity 14.9%;
   N50029;
04-SEP-1991 (first entry)
  antiproliferative; ss.
  1..501
   stability. They --- 501 BP;
     Bell LD, Boseley P
WPI; 85-311944/50.
   P-PSDB; P50022.
```

Homo sapiens.

RESULT
1D NS
AC NS
DT 04
DE Se
DE IF
KW AN
OS HC
FH KE
FT CI

/\*tag= a

ä

4; Caps

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/*tag=
CDS
   타타
  166 gcnytbacnathtaygaratgytbcaraayathttygcnathttymgdcargaywnnwnn 225
  410 SNWSNGAYCAYYTNYTNCCNGCNACNGARGARGCNCCNAARGTNTGYGARGCNTGYAARA 469
  226 wnnacnggntggaaygaracnathgtngaraayytbytbgcnaaygtn-taycaycarat 284
   285 haaycayytbaaracngtnytbgargaraarytbgaraargargayttyacnmgdggnaa 344
   345 rytbatgwnnwnnytbcayytbaarmgdtaytayggnmgdathytbcaytayytbaatgc 404
  405 naargattaywnncattgygcntggacnathgtnmgdgtngarathytbmgdaayttyta 464
  1; Gaps
  anti-proliferative and immune regulating actions Claim 28; Chart 2b, page 33; 71pp; English.

Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities for eal surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 110 A; 32 C; 66 G; 81 T;
   Sequence encoding new modified human beta interferon polypeptides
  New modified human beta interferón polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral,
   Query Match 7.1%; Score 49; DB 3; Length 501; Best Local Similarity 16.0%; Pred. No. 8.62e-05; Matches 50; Conservative 94; Mismatches 168; Indels
  Antiviral; cell growth regulator; immune system regulator; antiproliferative; 88.
  Location/Qualifiers
                                      Location/Qualifiers 1..501
   (SEAR ) SEARLE G D & CO.
Bell LD, Boseley PG, Porter AG,
WPI; 85-311944/50.
  N50032 standard; DNA; 501 BP
  04-SEP-1991 (first entry)
   /*tag= a
EP-163993-A.
17-DEC-1985, 105750,
17-MAY-1984, GB-012564.
   465 yttyathaaymgd 477
   710 AYYTNGTNATGGG 722
      antiproliferative; ss.
   P-PSDB; P50023
  Homo sapiens.
                         Homo sapiens.
   FNX 449
  RESULT
1D N5
AC N5
DT 04
DE Se
DE IF
KW AN
KW AN
COS H0
FH Ke
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Claim 28; Chart 2c, page 34; 71pp; English.
Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 112 A; 30 C; 69 G; 85 T; New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions Antiviral; cell growth regulator; immune system regulator; Location/Qualifiers 1..501 17-MAY-1984; GB-012564. (SEAR.) SEARLE G D 6 CO. BB-11 LLD, Boseley PG, Porter AG; WPI; 85-311944/50. P-PSDB; P50024. antiproliferative; ss. 17-MAY-1985; 105750 Homo sapiens. /\*tag= a EP-163993-A. 11-DEC-1985. Dec 9 10:15

DE PET THE PET

ä 4; Gaps Query Match 7.1%; Score 49; DB 3; Length 501; Best Local Similarity 15.7%; Pred. No. 8.62e-05; Aatches 71; Conservative 134; Mismatches 242; Indels

53 araarytbytbtggcarytbaayggnmgdytbgartaytgyytbaatgaymgdatgaayt 112 В

113 tygayathccncatgargarttygayggnaaycarttycaraargargaygcngcnytba 172გ

608 PTRTANATNGTYTTNWSYTTNGTYTCNARNATNATYTTNGTRTCNCKRTTNATRTANGTN 549 셤 გ

173 cnathtaygaratgytbcataayathttygcnathttymgdcatgaywnnwnnwnnacng 232 -:: :: 셤

233 gntggaaygaracnathgtngaraayytbytbgcnaaygtntaycaycarathaaycayy 292 548 ATYTCYTINACYTINATYTINARNGCRAARTCRITYTIRCANARNGTYTCCATNAIRTCR 489 გ 쇰

488 TTRICRICRICRITYTTRITYTTRCANGCYICRCANACYTINGGNGCYICYTCNGINGCN 429

გ g

293 tbaaracngtnytbgargara--arytbgaraa-rgargarttyacnmgdggnaarytba 349 : || :| :: :: || :: :: || 369

> გ 염 გ. 음 გ

tgwnnwnnytbcayytbaarmgdtaytayggnmgdathytbcaytayytbaargcnaatg 409 320

410 artaywnncattgygcntggacnathgtnmgdgtngarathytbmgdaayttytayttya 469

308 TCYTTNACYTGNACRCANARNWSRTGRCANGGYTGNATNGTYTCRTCNARRTCRTCNARR 249

470 thaaymgdytbacnggntay-ytbmgdaayt 499 염

248 CANACNGGNGCRAANARNWSRCANARRAAYT 218

S